WEST Search History

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DATE: Thursday, February 15, 2007

Hide?	Set Name	Query	Hit Count
		DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=OR	
☐	L10	CXCR4 NEAR (antibody or antibodies) AND (vascularization OR neovascularization OR vascularize)	271
☐	L9	L8 AND (vascularization OR neovascularization OR vascularize)	11
☐	L8	L6 AND (seven-transmembrane)	42
☐	L7	L6 AND (leaukocyte-derived)	0
☐	L6	LESTR AND antibody AND cancer	147
☐	L5	PF4A AND IL-8 AND antibody AND (vascularization OR neovascularization OR vascularize)	3
☐	L3	L2 AND antibody	23
☐	L2	PF4A AND IL-8 AND tumor	23
☐	L1	PF4A AND IL-8 AND cancer	6

END OF SEARCH HISTORY

SCORE Search Results Details for Application 10785230 and Search Result 20070206_074028_us-10-785-230-1.rai.

This page gives you Search Results detail for the Application 10785230 and Search Result 20070206_074028_us-10-785-230-1.rai.

start | next page

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GenCore version 6.2

OM protein - protein search, using sw model

Run on: February 6, 2007, 14:23:25 ; Search time 38 Seconds
(without alignments)
808.237 Million cell updates/sec

Title: US-10-785-230-1
Perfect score: 1830
Sequence: 1 MEGISIYTSDNYTEEMGSGD.....KRGGHSSVSTESESSSFHSS 352

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1830	100.0	352	1	US-08-202-056-3	Sequence 3, Appli
2	1830	100.0	352	1	US-08-076-093A-4	Sequence 4, Appli
3	1830	100.0	352	1	US-08-701-265-4	Sequence 4, Appli
4	1830	100.0	352	1	US-08-284-586-4	Sequence 4, Appli
5	1830	100.0	352	1	US-08-805-478-4	Sequence 4, Appli
6	1830	100.0	352	1	US-08-802-627A-4	Sequence 4, Appli
7	1830	100.0	352	1	US-08-801-238-4	Sequence 4, Appli
8	1830	100.0	352	1	US-08-801-228-4	Sequence 4, Appli
9	1830	100.0	352	2	US-09-104-296-4	Sequence 4, Appli

10	1830	100.0	352	2	US-09-517-605-4	Sequence 4, Appli
11	1830	100.0	352	2	US-09-647-501-2	Sequence 2, Appli
12	1824	99.7	352	2	US-09-826-509-485	Sequence 485, App
13	1789	97.8	352	1	US-08-450-393A-6	Sequence 6, Appli
14	1789	97.8	352	2	US-08-446-669-6	Sequence 6, Appli
15	1789	97.8	352	2	US-09-625-573-6	Sequence 6, Appli
16	1789	97.8	352	5	PCT-US95-00476-6	Sequence 6, Appli
17	1752	95.7	337	1	US-08-153-848-46	Sequence 46, Appl
18	1752	95.7	337	2	US-09-299-843A-46	Sequence 46, Appl
19	1752	95.7	337	2	US-09-088-337B-46	Sequence 46, Appl
20	1752	95.7	337	5	PCT-US93-11153-46	Sequence 46, Appl
21	614	33.6	116	2	US-09-513-999C-5992	Sequence 5992, Ap
22	600.5	32.8	360	2	US-08-875-573-20	Sequence 20, Appl
23	600.5	32.8	360	2	US-09-232-878-2	Sequence 2, Appli
24	600.5	32.8	360	2	US-09-045-583-55	Sequence 55, Appl
25	600.5	32.8	360	2	US-09-534-185-55	Sequence 55, Appl
26	600.5	32.8	360	2	US-08-939-107-34	Sequence 34, Appl
27	600.5	32.8	360	2	US-10-039-659A-16	Sequence 16, Appl
28	600.5	32.8	360	2	US-09-067-447B-34	Sequence 34, Appl
29	600.5	32.8	360	2	US-09-837-446-2	Sequence 2, Appli
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31	600.5	32.8	360	2	US-09-796-744-17	Sequence 17, Appl
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33	594	32.5	123	2	US-08-513-974B-330	Sequence 330, App
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35	588.5	32.2	360	2	US-09-938-719-10	Sequence 10, Appl
36	588.5	32.2	360	2	US-09-939-226B-10	Sequence 10, Appl
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39	576.5	31.5	368	2	US-08-829-839-2	Sequence 2, Appli
40	576.5	31.5	368	2	US-09-170-496D-20	Sequence 20, Appl
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44	572.5	31.3	368	2	US-09-170-496D-174	Sequence 174, App
45	569	31.1	367	2	US-10-244-089-2	Sequence 2, Appli

ALIGNMENTS

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RESULT 1
US-08-202-056-3
; Sequence 3, Application US/08202056
; Patent No. 5440021
;  GENERAL INFORMATION:
;    APPLICANT:  Chuntharapai, Anan
;    APPLICANT:  Hebert, Caroline
;    APPLICANT:  Kim, Kyung Jin
;    APPLICANT:  Lee, James
;    TITLE OF INVENTION:  Antibodies to Human IL-8 Type B Receptor
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/202,056
;      FILING DATE:  25-FEB-1994
;      CLASSIFICATION:  436
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/677211
;      FILING DATE:  29-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  706P3
;    TELECOMMUNICATION INFORMATION:
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;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  352 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-202-056-3

  Query Match             100.0%;  Score 1830;  DB 1;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-143;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
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Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
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Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
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Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
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Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 2
US-08-076-093A-4
; Sequence 4, Application US/08076093A
; Patent No. 5543503
;  GENERAL INFORMATION:
;    APPLICANT:  Chuntharapai, Anan
;    APPLICANT:  Lee, James
;    APPLICANT:  Hebert, Caroline
;    APPLICANT:  Jin Kim, K.
;    TITLE OF INVENTION:  Antibodies to Human PF4A Receptors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/076,093A
;      FILING DATE:  11-Jun-1993
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/810782
;      FILING DATE:  19-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/677211
;      FILING DATE:  29-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  706P2
```

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;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  352 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-076-093A-4

  Query Match             100.0%;  Score 1830;  DB 1;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-143;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
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Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
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Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
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Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
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Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 3
US-08-701-265-4
; Sequence 4, Application US/08701265
; Patent No. 5776457
;  GENERAL INFORMATION:
;    APPLICANT:  Chuntharapai, Anan
;    APPLICANT:  Lee, James
;    APPLICANT:  Hebert, Caroline
;    APPLICANT:  Jin Kim, K.
;    TITLE OF INVENTION:  Antibodies to Human PF4A Receptors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/701,265
;      FILING DATE:  22-AUG-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/076093
;      FILING DATE:  11-Jun-1993
;      APPLICATION NUMBER:  07/810782
;      FILING DATE:  19-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/677211
;      FILING DATE:  29-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
```

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;      NAME:  Love, Richard B
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  706P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  352 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-701-265-4

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  Best Local Similarity  100.0%;  Pred. No. 3.8e-143;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
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Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
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Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
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RESULT 4
US-08-284-586-4
; Sequence 4, Application US/08284586
; Patent No. 5840856
;  GENERAL INFORMATION:
;    APPLICANT:  Chuntharapai, Anan
;    APPLICANT:  Lee, James
;    APPLICANT:  Hebert, Caroline
;    APPLICANT:  Jin Kim, K.
;    TITLE OF INVENTION:  Antibodies to Human PF4A Receptors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/284,586
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/076,093A
;      FILING DATE:  11-Jun-1993
;      APPLICATION NUMBER:  07/810782
;      FILING DATE:  19-DEC-1991
;    PRIOR APPLICATION DATA:
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;       APPLICATION NUMBER:  07/677211
;       FILING DATE:  29-MAR-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Love, Richard B
;       REGISTRATION NUMBER:  34,659
;       REFERENCE/DOCKET NUMBER:  706P2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415/225-5530
;       TELEFAX:  415/952-9881
;       TELEX:  910/371-7168
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  352 amino acids
;       TYPE:  Amino Acid
;       TOPOLOGY:  Linear
US-08-284-586-4

  Query Match             100.0%;  Score 1830;  DB 1;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-143;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
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Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
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Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
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Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
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Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
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RESULT 5
US-08-805-478-4
; Sequence 4, Application US/08805478
; Patent No. 5874543
;  GENERAL INFORMATION:
;    APPLICANT:  Chuntharapai, Anan
;    APPLICANT:  Lee, James
;    APPLICANT:  Hebert, Caroline
;    APPLICANT:  Jin Kim, K.
;    TITLE OF INVENTION:  ANTIBODIES TO PF4A RECEPTOR
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/805,478
;      FILING DATE:  25-Feb-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/284586
;      FILING DATE:  10-AUG-1994
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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/076093
;      FILING DATE:  11-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/810782
;      FILING DATE:  19-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P0706P2P1C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  352 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-805-478-4

  Query Match             100.0%;  Score 1830;  DB 1;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-143;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 6
US-08-802-627A-4
; Sequence 4, Application US/08802627A
; Patent No. 5892017
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, James
;    APPLICANT:  Wood, William I.
;    TITLE OF INVENTION:  NUCLEIC ACID ENCODING PF4A RECEPTOR
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/802,627A
;      FILING DATE:  19-Feb-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
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;      APPLICATION NUMBER:  08/284586
;      FILING DATE:  10-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/076093
;      FILING DATE:  11-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/810782
;      FILING DATE:  19-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P0706P2P1D2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  352 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-802-627A-4

  Query Match             100.0%;  Score 1830;  DB 1;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-143;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 7
US-08-801-238-4
; Sequence 4, Application US/08801238
; Patent No. 5919896
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, James
;    APPLICANT:  Wood, William I.
;    TITLE OF INVENTION:  PF4A RECEPTOR
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/801,238
;      FILING DATE:  19-Feb-1997
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;       CLASSIFICATION: 530
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/284586
;       FILING DATE:  10-AUG-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/076093
;       FILING DATE:  11-JUN-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/810782
;       FILING DATE:  19-DEC-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Love, Richard B.
;       REGISTRATION NUMBER:  34,659
;       REFERENCE/DOCKET NUMBER:  P0706P2P1D1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415/225-5530
;       TELEFAX:  415/952-9881
;       TELEX:  910/371-7168
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  352 amino acids
;       TYPE:  Amino Acid
;       TOPOLOGY:  Linear
US-08-801-238-4

  Query Match             100.0%;  Score 1830;  DB 1;  Length 352;
  Best Local Similarity.  100.0%;  Pred. No. 3.8e-143;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 8
US-08-801-228-4
; Sequence 4, Application US/08801228
; Patent No. 5922541
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, James
;    APPLICANT:  Wood, William I.
;    TITLE OF INVENTION:  METHODS FOR DETECTION AND AMPLIFICATION OF
;    TITLE OF INVENTION:  PF4A RECEPTOR NUCLEIC ACID
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/801,228
;      FILING DATE:  19-Feb-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/284586
;      FILING DATE:  10-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/076093
;      FILING DATE:  11-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/810782
;      FILING DATE:  19-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P0706P2P1D3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  352 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-801-228-4

  Query Match             100.0%;  Score 1830;  DB 1;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-143;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
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Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 9
US-09-104-296-4
; Sequence 4, Application US/09104296
; Patent No. 6087475
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, James
;    APPLICANT:  Wood, WIlliam I.
;    TITLE OF INVENTION:  PF4A Receptors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
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;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  WinPatin (Genentech)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/104,296
;       FILING DATE:  24-June-1998
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/701265
;       FILING DATE:  22-AUG-1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/664228
;       FILING DATE:  06-JUN-1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/076093
;       FILING DATE:  11-JUN-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/810782
;       FILING DATE:  19-DEC-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Love, Richard B.
;       REGISTRATION NUMBER:  34,659
;       REFERENCE/DOCKET NUMBER:  P0706P2C2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415/225-5530
;       TELEFAX:  415/952-9881
;       TELEX:  910/371-7168
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  352 amino acids
;       TYPE:  Amino Acid
;       TOPOLOGY:  Linear
US-09-104-296-4

  Query Match             100.0%;  Score 1830;  DB 2;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-143;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 10
US-09-517-605-4
; Sequence 4, Application US/09517605
; Patent No. 6391567
; GENERAL INFORMATION:
;  APPLICANT: Littman, Dan R.
;  APPLICANT: Kwon, Douglas S.
;  APPLICANT: van Kooyk, Yvette
;  APPLICANT: Geijtenbeck, Tneo
;  TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
;  TITLE OF INVENTION: CELLS
;  FILE REFERENCE: 1049-1-017
;  CURRENT APPLICATION NUMBER: US/09/517,605
;  CURRENT FILING DATE: 2000-03-02
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;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-517-605-4

  Query Match             100.0%;  Score 1830;  DB 2;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-143;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 11
US-09-647-501-2
; Sequence 2, Application US/09647501
; Patent No. 6863887
; GENERAL INFORMATION:
;  APPLICANT: No. 6863887thwest Biotherapeutics, Inc.
;  APPLICANT:  Murphy, Gerald P.
;  APPLICANT:  Boynton, Alton L.
;  APPLICANT:  Sehgal, Anil
;  TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED ON THE
;  TITLE OF INVENTION:  ROLE OF THE CXCR-4 GENE IN TUMORIGENESIS
;  FILE REFERENCE: 20093-000600PC
;  CURRENT APPLICATION NUMBER: US/09/647,501
;  CURRENT FILING DATE:  2000-09-24
;  PRIOR APPLICATION NUMBER: 60/079,916
;  PRIOR FILING DATE: 1998-03-30
;  PRIOR APPLICATION NUMBER: 60/104,656
;  PRIOR FILING DATE: 1998-10-16
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-647-501-2

  Query Match             100.0%;  Score 1830;  DB 2;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-143;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
                ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 12
US-09-826-509-485
; Sequence 485, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
;  APPLICANT: Lehmann-Bruinsma, Karin
;  APPLICANT:  Liaw, Chen W.
;  APPLICANT:  Lin, I-Lin
;  TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
;  TITLE OF INVENTION:  Protein-Coupled Receptors
;  FILE REFERENCE: AREN-207
;  CURRENT APPLICATION NUMBER: US/09/826,509
;  CURRENT FILING DATE:  2001-04-05
;  PRIOR APPLICATION NUMBER: 60/195,747
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: 09/170,496
;  PRIOR FILING DATE: 1998-10-13
;  NUMBER OF SEQ ID NOS: 589
;  SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 485
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-826-509-485

  Query Match             99.7%;  Score 1824;  DB 2;  Length 352;
  Best Local Similarity   99.7%;  Pred. No. 1.2e-142;
  Matches  351;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAKKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
                ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 13
US-08-450-393A-6
; Sequence 6, Application US/08450393A
; Patent No. 5707815
;  GENERAL INFORMATION:
;    APPLICANT:  Charo, Israel
```

```
;    APPLICANT:  Coughlin, Shaun
;    TITLE OF INVENTION:  MAMMALIAN MONOCYTE CHEMOATTRACTANT
;    TITLE OF INVENTION:  PROTEIN RECEPTORS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooley Godward Castro Huddleson & Tatum
;      STREET:  5 Palo Alto Square
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94306-2155
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/450,393A
;      FILING DATE:  May 25, 1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cserr, Luann
;      REGISTRATION NUMBER:  31,822
;      REFERENCE/DOCKET NUMBER:  UCAL-237/02US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-843-5165
;      TELEFAX:  415-8857-0663
;      TELEX:  380816CooleyPA
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  352 amino acids
;      TYPE:  amino acid
```

SCORE Search Results Details for Application 10785230 and Search Result 20070206_074015_us-10-785-230-1.rag.

This page gives you Search Results detail for the Application 10785230 and Search Result 20070206_074015_us-10-785-230-1.rag.

start | next page

Go Back to previous page

GenCore version 6.2

OM protein - protein search, using sw model

Run on: February 6, 2007, 14:07:09 ; Search time 211 Seconds
(without alignments)
814.792 Million cell updates/sec

Title: US-10-785-230-1
Perfect score: 1830
Sequence: 1 MEGISIYTSDNYTEEMGSGD.....KRGGHSSVSTESESSSFHSS 352

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200701:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*
11: geneseqp2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1830	100.0	352	2	AAR68812	Aar68812 Human mon
2	1830	100.0	352	2	AAR80757	Aar80757 Chemokine
3	1830	100.0	352	2	AAY39993	Aay39993 Human CXC
4	1830	100.0	352	3	AAY52507	Aay52507 Human CXC
5	1830	100.0	352	4	AAE06690	Aae06690 Human neu

6	1830	100.0	352	4	AAG79088	Aag79088 Amino aci
7	1830	100.0	352	4	AAG80123	Aag80123 Human CXC
8	1830	100.0	352	5	AAO14003	Aao14003 Human cys
9	1830	100.0	352	5	ABP52651	Abp52651 Human CXC
10	1830	100.0	352	5	ABG32977	Abg32977 Human CXC
11	1830	100.0	352	5	ABG33065	Abg33065 Human CXC
12	1830	100.0	352	5	ABP65183	Abp65183 Hypoxia-r
13	1830	100.0	352	5	AAG78471	Aag78471 CXCR4 pro
14	1830	100.0	352	6	ABP96794	Abp96794 Human COP
15	1830	100.0	352	6	ABU03495	Abu03495 Angiogene
16	1830	100.0	352	6	ABR58581	Abr58581 Human can
17	1830	100.0	352	6	ABP97733	Abp97733 Amino aci
18	1830	100.0	352	6	ABP81796	Abp81796 Human CXC
19	1830	100.0	352	7	ADC98646	Adc98646 Human CXC
20	1830	100.0	352	7	ADE63147	Ade63147 Human Pro
21	1830	100.0	352	7	ADE63143	Ade63143 Human Pro
22	1830	100.0	352	7	ADF90878	Adf90878 Human hep
23	1830	100.0	352	7	ADO16837	Ado16837 CXCR4 ami
24	1830	100.0	352	7	ADN95821	Adn95821 Human BEC
25	1830	100.0	352	8	ADH17079	Adh17079 Human orp
26	1830	100.0	352	8	ADN04756	Adn04756 Antipsori
27	1830	100.0	352	8	ADO29271	Ado29271 Human GPC
28	1830	100.0	352	8	ADP12477	Adp12477 Protein e
29	1830	100.0	352	8	ADP12926	Adp12926 Protein e
30	1830	100.0	352	8	ADP13001	Adp13001 Protein e
31	1830	100.0	352	8	ADO19692	Ado19692 Human PRO
32	1830	100.0	352	8	ADO19832	Ado19832 Human PRO
33	1830	100.0	352	8	ADO20013	Ado20013 Human PRO
34	1830	100.0	352	8	ADP44055	Adp44055 Human CXC
35	1830	100.0	352	8	ADQ14488	Adq14488 Human che
36	1830	100.0	352	8	ADQ97944	Adq97944 Human can
37	1830	100.0	352	8	ADR51540	Adr51540 Human lip
38	1830	100.0	352	8	ADR87598	Adr87598 Human CXC
39	1830	100.0	352	9	ADY19742	Ady19742 PRO polyp
40	1830	100.0	352	9	ADY16664	Ady16664 PRO polyp
41	1830	100.0	352	9	ADY17210	Ady17210 PRO polyp
42	1830	100.0	352	9	ADY16155	Ady16155 PRO polyp
43	1830	100.0	352	9	AED15419	Aed15419 Equine Pr
44	1830	100.0	352	9	AED76716	Aed76716 CXCR4 rec
45	1830	100.0	352	10	AEE66168	Aee66168 Human CXC

ALIGNMENTS

```
RESULT 1
AAR68812
ID   AAR68812 standard; protein; 352 AA.
XX
AC   AAR68812;
XX
DT   25-MAR-2003  (revised)
DT   18-JUL-1995  (first entry)
XX
DE   Human monocyte PF4AR.
XX
KW   Interleukin-8 receptor; IL-8 receptor; PF4AR;
KW   platelet factor superfamily receptor; monocyte; chemotactic;
KW   inflammation; inflammatory disease; arthritis; emphysema; cystic;
KW   fibrosis; colitis; bronchitis; meningitis; therapeutic.
XX
OS   Homo sapiens.
XX
PN   WO9428931-A1.
XX
PD   22-DEC-1994.
XX
PF   07-JUN-1994;   94WO-US006380.
XX
PR   11-JUN-1993;   93US-00076093.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Chuntharapai A,  Lee J,  Hebert C,  Kim KJ;
XX
DR   WPI; 1995-036114/05.
```

```
DR   N-PSDB; AAQ80521.
XX
PT   Treatment of inflammatory disorders - by administering an antibody
PT   capable of binding a platelet factor 4 superfamily receptor polypeptide.
XX
PS   Disclosure; Page 54-56; 83pp; English.
XX
CC   2 PF4AR members were identified by probing lambda libraries from human
CC   monoclyte-like cell line HL-60 and human peripheral blood lymphocytes
CC   using a large fragment of IL-8 receptor DNA (full sequence given in
CC   AAQ80520). The nucleotide sequences of the 2 PF4ARs are given in AAQ80521
CC   and AAQ80522, and their respective amino acid sequences in AAR68812 and
CC   AAR68813. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 352 AA;

  Query Match             100.0%;  Score 1830;  DB 2;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-213;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 2
AAR80757
ID   AAR80757 standard; protein; 352 AA.
XX
AC   AAR80757;
XX
DT   25-MAR-2003  (revised)
DT   26-MAR-1996  (first entry)
XX
DE   Chemokine superfamily receptor.
XX
KW   Interleukin; IL-8; inflammation; psoriasis; dermatitis;
KW   rheumatoid arthritis; inflammatory bowel disease;
KW   chronic lung inflammation; treatment; antibody; affinity purification;
KW   detection.
XX
OS   Homo sapiens.
XX
PN   US5440021-A.
XX
PD   08-AUG-1995.
XX
PF   25-FEB-1994;   94US-00202056.
XX
PR   29-MAR-1991;   91US-00677211.
XX
PA   (HEBE/) HEBERT C.
PA   (CHUN/) CHUNTHARAPAI A.
PA   (KIMK/) KIM K J.
PA   (LEEJ/) LEE J.
XX
```

PI Chuntharapai A, Kim KJ, Hebert C, Lee J;
XX
DR WPI; 1995-283151/37.
DR N-PSDB; AAQ99007.
XX
PT New antibodies against interleukin 8 type B receptor - used to treat or
PT prevent inflammation, also for detecting receptor expression and
PT purificn.
XX
PS Example 2; Col 45-48; 62pp; English.
XX
CC Antibodies directed against the interleukin-8 receptor B can be used to
CC treat or prevent inflammation e.g. psoriasis, dermatitis, rheumatoid
CC arthritis and particularly inflammatory bowel disease and chronic lung
CC inflammation. When immobilised, these antibodies may be used to detect
CC interleukin-8 receptor B expression in cells and tissues and for affinity
CC purification of interleukin-8 receptor B from cells. This sequence is an
CC additonal chemokine superfamily receptor which was identified by probing
CC lamda libraries of genomic DNA from a human monocyte-like cell line (L-
CC 60) and human peripheral blood lymphocytes using a large fragment of the
CC interleukin-8 type A receptor DNA (See AAQ99006). (Updated on 25-MAR-2003
CC to correct PF field.)
XX
SQ Sequence 352 AA;

  Query Match   100.0%; Score 1830; DB 2; Length 352;
  Best Local Similarity 100.0%; Pred. No. 2.7e-213;
  Matches 352; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
```

RESULT 3
AAY39993
ID AAY39993 standard; protein; 352 AA.
XX
AC AAY39993;
XX
DT 16-DEC-1999 (first entry)
XX
DE Human CXCR4 protein sequence.
XX
KW CXCR4; human; neovascularisation; inhibitor; solid cancer; therapy;
KW tissue repairing agent; vascularisation.
XX
OS Homo sapiens.
XX
PN WO9948528-A1.
XX
PD 30-SEP-1999.
XX
PF 23-MAR-1999; 99WO-JP001448.
XX
PR 24-MAR-1998; 98JP-00095448.

XX
PA (CHUS) CHUGAI SEIYAKU KK.
PA (KISH/) KISHIMOTO T.
XX
PI Kishimoto T, Nagasawa T, Tachibana K;
XX
DR WPI; 1999-591042/50.
DR N-PSDB; AAZ27610.
XX
PT CXCR4-potentiating agents and methods useful for inhibiting
PT neovascularization, and treating solid cancers.
XX
PS Disclosure; Page 47-48; 63pp; Japanese.
XX
CC This sequence is the human CXCR4 protein. The invention relates to
CC remedies inhibiting neovascularisation, remedies for solid cancer,
CC remedies for diseases pathologically caused by neovascularisation and
CC tissue repairing agents containing as the active ingredient a substance
CC capable of potentiating CXCR4. Based on a finding that vascularisation is
CC inhibited in a CXCR4 knockout mouse, it becomes possible to prepare
CC remedies inhibiting vascularisation which contain as the active
CC ingredient a substance capable of potentiating CXCR4, remedies for solid
CC cancer, remedies for diseases pathologically caused by neovascularisation
CC and tissue repairing agents containing as the active ingredient a
CC substance capable of potentiating CXCR4. It is also possible to establish
CC methods for treatment with the use of these remedies
XX
SQ Sequence 352 AA;

Query Match 100.0%; Score 1830; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.7e-213;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
```

RESULT 4
AAY52507
ID AAY52507 standard; protein; 352 AA.
XX
AC AAY52507;
XX
DT 22-FEB-2000 (first entry)
XX
DE Human CXC-chemokine receptor-4 (CXCR-4).
XX
KW CXC-chemokine receptor-4; CXCR-4; stromal cell derived factor-1; SDF-1;
KW ligand; chemotaxis; inflammation; G-protein-coupled receptor;
KW signal transduction; CD4-independent; HIV-1; infection; proliferation;
KW transformation; tumorigenesis; cancer; tumour; overexpression; brain;
KW breast; colon; lung; melanoma; glioblastoma; inhibition; growth arrest;
KW diagnosis; prognosis; marker; proliferative disorders; antisense;
KW therapy; treatment; premalignant condition; hypertrophy;
KW degenerative disorder; Parkinson's disease; Alzheimer's disease;

KW growth deficiency; hypoproliferative disorder; physical trauma; lesion;
KW ischaemia; wound.
XX
OS Homo sapiens.
XX
PN WO9950461-A1.
XX
PD 07-OCT-1999.
XX
PF 29-MAR-1999; 99WO-US007431.
XX
PR 30-MAR-1998; 98US-0079916P.
PR 16-OCT-1998; 98US-0104656P.
XX
PA (NWBI-) NORTHWEST BIOTHERAPEUTICS INC.
XX
PI Murphy GP, Boynton AL, Sehgal A;
XX
DR WPI; 2000-052634/04.
DR N-PSDB; AAZ38553.
XX
PT Use of CXCR-4 and SDF-1 as markers for diagnosis and treatment of e.g.
PT tumors, degenerative disorders, growth deficiencies, hyper- and
PT hypoproliferative disorders, physical trauma, lesions and wounds.
XX
PS Disclosure; Fig 14; 138pp; English.
XX
CC This sequence represents CXC-chemokine receptor-4 (CXCR-4). Chemokine
CC receptors play an important role in the chemotaxis of T-cells and
CC phagocytic cells to areas of inflammation. CXCR-4 is a member of the G-
CC protein-coupled receptor family, which is involved in signal
CC transduction, and its ligand is stromal cell derived factor-1 (SDF-1,
CC AAY52508). CXCR-4 also mediates CD4-independent infection by HIV-1. CXCR-
CC 4 has now been found to have a role in the aberrant proliferative
CC behaviour of a number of cell types, including numerous primary tumours
CC and derived cell lines. CXCR-4 is involved in cell transformation and
CC tumorigenesis, particularly in brain, breast and colon tumours. It was
CC found to be overexpressed in several brain tumour derived cell lines and
CC primary brain tumour tissues, breast tumour tissues, colorectal
CC adenocarcinoma, lung carcinoma and melanoma cell lines. CXCR-4 expression
CC was required for the continuous proliferation of glioblastoma cancer
CC cells, and inhibition of its gene function resulted in growth arrest.
CC Conversely, overexpression resulted in enhanced and rapid cellular
CC proliferation. CXCR-4 and SDF-1 can be used as markers for the diagnosis
CC and prognosis of cell proliferative disorders, and antisense
CC oligonucleotides complementary to at least a portion of an RNA transcript
CC of a CXCR-4 gene can be used to inhibit hyperproliferation of a tumour
CC cell. Agents that inhibit CXCR-4 function can be used for treating or
CC preventing a disease or disorder involving cell overproliferation, e.g.,
CC brain cancer, breast cancer, colon cancer, prostate cancer and B cell
CC lymphoma, and also premalignant conditions, benign tumours,
CC hyperproliferative disorders, and benign dysproliferative disorders. They
CC can also be used for treating e.g., cirrhosis of the liver, keloid
CC formation, psoriasis, benign tumors, fibrocystic conditions and tissue
CC hypertrophy. Compounds that promote CXCR-4 function can also be used for
CC preventing or treating a disease or disorder involving a deficiency in
CC cell proliferation, or treating a condition where cell proliferation
CC would be desirable. Such diseases include degenerative disorders (e.g.,
CC Parkinson's disease, Alzheimer's disease), growth deficiencies,
CC hypoproliferative disorders, physical trauma, lesions (e.g., those caused
CC by ischaemia), and wounds
XX
SQ Sequence 352 AA;

Query Match 100.0%; Score 1830; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.7e-213;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
```

```
Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
```

RESULT 5
AAE06690
ID AAE06690 standard; protein; 352 AA.
XX
AC AAE06690;
XX
DT 16-OCT-2001 (first entry)
XX
DE Human neuropeptide Y (NPY) Y3 receptor.
XX
KW Human; neuropeptide Y; NPY; bone disease; bone mass; gene therapy;
KW cerebrospinal fluid; CSF; inositol phosphate; IP; Paget's disease;
KW fracture; extracellular signal-regulated kinase; ERK; osteoporosis;
KW osteopenia; bone metastasis; neurotransmitter; osteogenic;
KW NPY Y3 receptor.
XX
OS Homo sapiens.
XX
PN WO200153477-A1.
XX
PD 26-JUL-2001.
XX
PF 22-JAN-2001; 2001WO-US002040.
XX
PR 20-JAN-2000; 2000US-00489872.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (AMLI/) AMLING M.
XX
PI Amling M, Karsenty G, Ducy P;
XX
DR WPI; 2001-488709/53.
DR N-PSDB; AAD12801.
XX
PT Treating or preventing reduced bone mass, e.g. osteoporosis, by reducing
PT the level of neuropeptide Y activity in blood or cerebrospinal fluid.
XX
PS Example 7; Page 85; 102pp; English.
XX
CC The present invention relates to a method for treatment or prevention of
CC bone diseases characterised by loss of bone mass, comprises administering
CC to a mammal a compound that lowers the level of neuropeptide Y (NPY) in
CC the serum or cerebrospinal fluid (CSF) or a compound that lowers the
CC level of inositol phosphate (IP) or extracellular signal-regulated kinase
CC (ERK). The method is specifically used to treat (including by gene
CC therapy) or prevent osteoporosis, osteopenia or Paget's disease, but may
CC also be used e.g., in cases of fractures or bone metastases. These
CC diseases may also be diagnosed by detecting elevated NPY levels,
CC including monitoring of treatment, assessing efficacy of compounds in
CC clinical trials and for identifying subjects at risk. The present
CC sequence is a human NPY Y3 receptor
XX
SQ Sequence 352 AA;

```
  Query Match             100.0%;  Score 1830;  DB 4;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-213;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
                ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
```

RESULT 6
AAG79088
ID. AAG79088 standard; protein; 352 AA.
XX
AC AAG79088;
XX
DT 10-DEC-2001 (first entry)
XX
DE Amino acid sequence of human CXCR4 protein.
XX
KW Human; receptor; DC-SIGN; dendritic cell; T lymphocyte; HIV; gp120;
KW C-type lectin; ICAM3; HIV entry; T cell; macrophage; HIV infection;
KW CXCR4.
XX
OS Homo sapiens.
XX
PN WO200164752-A2.
XX
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US006322.
XX
PR 02-MAR-2000; 2000US-00517605.
XX
PA (UYNY) UNIV NEW YORK STATE.
PA (UYNI-) UNIV NIJMEGEN.
XX
PI Littman DR, Kwon D, Van Kooyk Y, Geijtenbeek T;
XX
DR WPI; 2001-602565/68.
XX
PT An antibody for the treatment or prevention of HIV-infection comprises a
PT gp120 portion which binds to DC-SIGN or is exposed upon gp120 binding of
PT DC-SIGN due to concomitant conformational change.
XX
PS Disclosure; Page 117-118; 131pp; English.
XX
CC The specification describes an antibody which is specific for an
CC antigenic fragment of gp120. This antigenic fragment binds to DC-SIGN or
CC is exposed upon gp120 binding of DC-SIGN due to concomitant
CC conformational change. DC-SIGN is a receptor that is specifically
CC expressed on dendritic cells and facilitates infection of T lymphocytes
CC with HIV. DC-SIGN is identical to a HIV-1 gp120-binding C-type lectin. DC
CC -SIGN binds ICAM-3 (which is expressed constitutively on T lymphocytes)
CC with high affinity. The antibody of the invention inhibits the trans
CC enhancement of HIV entry into a T cell or macrophage facilitated by
CC dendritic cells. The antibody is useful to treat or prevent HIV
CC infection. The present sequence represents a human CXCR4 protein, which
CC is a translocation promoting agent that interacts with CD4. This receptor
CC functions in HIV-1 entry into cells
XX
SQ Sequence 352 AA;

Query Match 100.0%; Score 1830; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.7e-213;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
```

RESULT 7
AAG80123
ID AAG80123 standard; protein; 352 AA.
XX
AC AAG80123;
XX
DT 17-JAN-2002 (first entry)
XX
DE Human CXCR4 protein.
XX
KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;
KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
KW antirheumatic; antiarthritic.
XX
OS Homo sapiens.
XX
PN WO200172830-A2.
XX
PD 04-OCT-2001.
XX
PF 02-APR-2001; 2001WO-EP003708.
XX
PR 31-MAR-2000; 2000DE-01016013.
XX
PA (IPFP-) IPF PHARM GMBH.
PA (FORS/) FORSSMANN U.
XX
PI Forssmann W, Adermann K, Heitland A, Spodsberg N;
XX
DR WPI; 2001-626256/72.
XX
PT Diagnostic agent containing two or more receptor-specific ligands, useful
PT for detecting tumors, inflammation etc., also therapeutic use of ligand
PT inhibitors.
XX
PS Disclosure; Page 12; 26pp; German.
XX
CC This invention describes a novel diagnostic agent (A) comprising at least
CC two different ligands (I) for receptors (II) that are implicated in
CC disease. (A) are used for the diagnosis of tumors (especially colorectal
CC or prostatic), organ rejection, inflammation and autoimmune diseases.
CC Also inhibitors of (I) are used therapeutically against tumors (and their
CC metastases), inflammation (particularly bronchial asthma or chronic bowel
CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),

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CC   where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
CC   endocrine, motor or urogenital systems or skin are affected, and bone
CC   marrow diseases. The products of the invention are chemokine derivatives
CC   which have cytostatic, antiinflammatory, antiasthmatic,
CC   immunosuppressive, dermatological, antirheumatic, antiarthritic.
CC   Chemokines act on specific tumor and inflammatory cells through a
CC   constellation of chemokine receptors (CR), which control migration and
CC   proliferation of these cells. AAG80045-AAG80128 represent human chemokine
CC   fragments used to illustrate the method of the invention
XX
SQ   Sequence 352 AA;

  Query Match             100.0%;  Score 1830;  DB 4;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-213;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 8
AAO14003
ID   AAO14003 standard; protein; 352 AA.
XX
AC   AAO14003;
XX
DT   08-MAY-2002  (first entry)
XX
DE   Human cysteine-X-cysteine chemokine receptor 4.
XX
KW   Cysteine-X-Cysteine Chemokine Receptor 4; CXCR4 binding peptide;
KW   chemoattractant cytokine; human immunodeficiency virus; HIV;
KW   HIV envelope glycoprotein; cellular CD4 receptor; env gene; gp160; gp120;
KW   gp41; CD4+ target cell; HIV-infected cell; CXCR4-binding compound;
KW   acquired immunodeficiency syndrome; AIDS; human; receptor.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .39
FT                   /note= "Extracellular N-terminus; this is involved in HIV
FT                   entry into a cell"
FT   Region          40. .64
FT                   /note= "Transmembrane segment 1 (TM1)"
FT   Region          65. .76
FT                   /note= "Intracellular loop 1"
FT   Region          77. .99
FT                   /note= "Transmembrane segment 2 (TM2)"
FT   Region          100. .110
FT                   /note= "Extracellular loop 1"
FT   Region          111. .131
FT                   /note= "Transmembrane segment 3 (TM3)"
FT   Region          132. .176
FT                   /note= "Intracellular loop 2"
FT   Region          177. .197
```

```
FT                   /note= "Transmembrane segment 4 (TM4)"
FT   Region          198. .203
FT                   /note= "Extracellular loop 2; required for HIV entry into
FT                   a cell"
FT   Region          204. .223
FT                   /note= "Transmembrane segment 5 (TM5)"
FT   Region          224. .240
FT                   /note= "Intracellular loop 3"
FT   Region          241. .261
FT                   /note= "Transmembrane segment 6 (TM6)"
FT   Region          262. .282
FT                   /note= "Extracellular loop 3; this is involved in HIV
FT                   entry into a cell"
FT   Binding-site    275
FT                   /note= "Binds HIV gp120"
FT   Binding-site    278
FT                   /note= "Binds HIV gp120"
FT   Misc-difference 280. .281
FT                   /note= "Apparently encoded by nucleotides 838-903 of
FT                   AAK98241"
FT   Region          283. .307
FT                   /note= "Transmembrane segment 7 (TM7)"
FT   Region          308. .352
FT                   /note= "Intracellular C-terminus"
XX
PN   WO200170768-A2.
XX
PD   27-SEP-2001.
XX
PF   21-MAR-2001; 2001WO-US009160.
XX
PR   21-MAR-2000; 2000US-0190946P.
PR   21-MAR-2000; 2000US-0190996P.
PR   21-MAR-2000; 2000US-0191299P.
PR   20-MAR-2001; 2001US-00813448.
PR   20-MAR-2001; 2001US-00813651.
PR   20-MAR-2001; 2001US-00813653.
XX
PA   (CONS-) CONSENSUS PHARM INC.
XX
PI   Nestor JJ, Wilson CJ,  Tan Hehir CA,  Kates SA;
XX
DR   WPI; 2002-010593/01.
DR   N-PSDB; AAK98241.
XX
PT   Identifying agents that bind to CXC chemokine receptor 4, useful for
PT   treatment and prevention of acquired immunodeficiency syndrome, comprises
PT   screening compound library for members that bind to the receptor.
XX
PS   Example 3; Fig 3B; 46pp; English.
XX
CC   The invention relates to a method of identifying Cysteine-X-Cysteine
CC   chemokine receptor 4 (CXCR4) binding compounds. The method comprises
CC   testing and selecting compounds in a library for their ability to bind to
CC   CXCR4. Chemokines (chemoattractant cytokines) regulate the movement and
CC   biological activities of leukocytes in many disease situations. CXCR4
CC   acts as a co-receptor for human immunodeficiency virus (HIV), as it
CC   interacts with the HIV envelope glycoproteins and the cellular CD4
CC   receptor, to facilitate HIV entry into cells. The HIV glycoproteins
CC   (encoded by the env gene) are translated as a precursor (gp160) which is
CC   subsequently cleaved into gp120 and gp41. Gp120 binds to CXCR4 and the
CC   CD4 receptor present on the surface of susceptible CD4+ target cells,
CC   causing the virus to fuse with the cell membranes and thereby
CC   facilitating entry of the virus into the cell. The eventual expression of
CC   the env product on the surface of the HIV-infected cell enables the cell
CC   to fuse with uninfected CD4+ cells, thereby spreading the infection. The
CC   CXCR4-binding compounds of the invention inhibit the entry of HIV into
CC   the CD4+ cell and therefore are useful in the prevention of HIV infection
CC   and the treatment and prevention of acquired immunodeficiency syndrome
CC   (AIDS). The present sequence represents the human CXCR4 protein used in
CC   the method of the invention
XX
SQ   Sequence 352 AA;

  Query Match             100.0%;  Score 1830;  DB 5;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-213;
```

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  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 9
ABP52651
ID   ABP52651 standard; protein; 352 AA.
XX
AC   ABP52651;
XX
DT   30-OCT-2002  (first entry)
XX
DE   Human CXC chemokine receptor 4 protein SEQ ID NO:126.
XX
KW   Cysteine-X-cysteine chemokine receptor 4; CXC chemokine receptor 4;
KW   binding; identification; AIDS; HIV; CXCR4; virucide; anti-HIV.
XX
OS   Homo sapiens.
XX
PN   WO200257313-A2.
XX
PD   25-JUL-2002.
XX
PF   26-OCT-2001; 2001WO-US051165.
XX
PR   27-OCT-2000; 2000US-0243587P.
PR   20-MAR-2001; 2001US-00813448.
PR   20-MAR-2001; 2001US-00813651.
PR   20-MAR-2001; 2001US-00813653.
XX
PA   (CONS-) CONSENSUS PHARM INC.
XX
PI   Nestor JJ,  Wilson CJ,  Tan Hehir CA,  Kates SA,  Krstenansky J;
XX
DR   WPI; 2002-608378/65.
DR   N-PSDB; ABQ74938.
XX
PT   Identifying a binding compound for cysteine-X-cysteine chemokine receptor
PT   4 (CXCR4) for preventing or treating AIDS and HIV infection, comprises
PT   binding a molecule to a molecule with a binding property corresponding to
PT   CXCR4.
XX
PS   Example 3; Fig 3A-B; 92pp; English.
XX
CC   The present invention describes a method (M1) for identifying a binding
CC   compound for cysteine-X-cysteine chemokine receptor 4 (CXCR4) comprises
CC   binding a molecule from the library of two or more molecules to the
CC   molecule with a binding property corresponding to CXCR4. (M1) comprises:
CC   (a) providing a library of two or more molecules; (b) providing a
CC   molecule with a binding property corresponding to CXCR4; (c) binding a
CC   molecule from the library of two or more molecules to the molecule with a
CC   binding property corresponding to CXCR4; (d) separating the bound
CC   molecule from the library of two or more molecules; and (e) identifying
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CC   the bound molecule as a binding compound for CXCR4. Also described is a
CC   binding compound (I) for CXCR4 identified from M1. (I) has virucide and
CC   anti-HIV activities. A partially purified CXCR4 protein is useful for
CC   carrying out selection, identification and improvement of tight binding
CC   ligands in identifying therapeutically useful compounds. Therapeutic
CC   peptides, peptidomimetics, or small molecule antagonists or agonists of
CC   CXCR4 binding may be used in the prevention and treatment of AIDS and HIV
CC   infection. The present sequence represents human CXCR4 which is given in
CC   an example from the present invention
XX
SQ   Sequence 352 AA;

  Query Match             100.0%;  Score 1830;  DB 5;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-213;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 10
ABG32977
ID   ABG32977 standard; protein; 352 AA.
XX
AC   ABG32977;
XX
DT   02-DEC-2002  (first entry)
XX
DE   Human CXC chemokine receptor 4 (CXCR4).
XX
KW   CXC chemokine receptor 4; CXCR4; chemotaxis induction; SDF1a;
KW   stromal cell-derived factor lalpha; angiogenesis; atherosclerosis;
KW   restenosis; ischaemic stroke; spinal cord injury; infection; ulcer;
KW   human immunodeficiency virus; HIV; acquired immunodeficiency syndrome;
KW   AIDS; pain; cancer; benign prostatic hypertrophy; diabetes; obesity;
KW   anorexia; bulimia; asthma; Parkinson's disease; acute heart failure;
KW   hypotension; hypertension; urinary retention; osteoporosis; stroke;
KW   anginal pectoris; myocardial infarction; benign prostatic hypertrophy;
KW   migraine; vomiting; psychotic disorder; neurological disorder; anxiety;
KW   schizophrenia; dyskinesia; Huntingdon's disease; restenosis;
KW   inflammatory disease; rheumatoid arthritis; diabetic retinopathy;
KW   inflammatory bowel disease; atherosclerosis; Alzheimer's disease;
KW   congestive heart failure; cardiac remodeling; angiogenic diseases;
KW   solid tumour; Kaposi Sarcoma; human.
XX
OS   Homo sapiens.
XX
PN   US2002107195-A1.
XX
PD   08-AUG-2002.
XX
PF   17-SEP-2001; 2001US-00953692.
XX
PR   21-JUL-1998;   98US-0093596P.
PR   21-JUL-1999;   99US-00358624.
```

XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Gupta SK;
XX
DR WPI; 2002-697879/75.
DR N-PSDB; ABS53992.
XX
PT Inducing chemotaxis of endothelial cells, useful for regulating
PT angiogenesis, e.g. for treating cancer, comprises treatment with stromal
PT cell-derived factor 1 alpha.
XX
PS Claim 3; Fig 1; 26pp; English.
XX
CC The invention describes a method of inducing chemotaxis of endothelial
CC cells by treatment with stromal cell-derived factor 1alpha (SDF1a). The
CC method is used for stimulating EC chemotaxis, and thus angiogenesis, and
CC is used for treating atherosclerosis, restenosis, ischaemic stroke and
CC spinal cord injury. Inhibition of this process is useful in treatment and
CC prevention of a very wide range of diseases, such as, infection (by
CC bacteria, fungi, protozoa or viruses such as human immunodeficiency virus
CC (HIV) and acquired immunodeficiency syndrome (AIDS)), pain, cancer and
CC benign prostatic hypertrophy, diabetes, obesity, anorexia, bulimia,
CC asthma, Parkinson's disease, acute heart failure, hypotension,
CC hypertension, urinary retention, osteoporosis, anginal pectoris,
CC myocardial infarction, stroke, ulcers, benign prostatic hypertrophy,
CC migraine, vomiting, psychotic and neurological disorders (e.g. anxiety,
CC schizophrenia) and dyskinesias (e.g. Huntingdon's disease), inflammatory
CC diseases, rheumatoid arthritis, diabetic retinopathy, inflammatory bowel
CC disease, atherosclerosis, restenosis, Alzheimer's disease, congestive
CC heart failure, cardiac remodeling, angiogenic diseases, solid tumours,
CC and Kaposi Sarcoma. This is the amino acid sequence of a CXC chemokine

start | next page

SCORE Search Results Details for Application 10785230 and Search Result 20070206_074020_us-10-785-230-1.rup.

This page gives you Search Results detail for the Application 10785230 and Search Result 20070206_074020_us-10-785-230-1.rup.

start | next page

Go Back to previous page

```
                    GenCore version 6.2
                Copyright (c) 1993 - 2007  Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:         February  6, 2007, 14:08:15 ; Search time 227 Seconds
                                        (without alignments)
                                        1660.742 Million cell updates/sec

Title:          US-10-785-230-1
Perfect score:  1830
Sequence:       1 MEGISIYTSDNYTEEMGSGD.........KRGGHSSVSTESESSSFHSS 352

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters:      3281787

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       UniProt_8.4:*
                1:  uniprot_sprot:*
                2:  uniprot_trembl:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                    SUMMARIES
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Result No.	Score	% Query Match	Length	DB	ID	Description
1	1830	100.0	352	1	CXCR4_HUMAN	P61073 homo sapien
2	1830	100.0	352	1	CXCR4_PANTR	P61072 pan troglod
3	1830	100.0	352	2	Q53S69_HUMAN	Q53s69 homo sapien
4	1822	99.6	352	2	Q9BXA0_HUMAN	Q9bxa0 homo sapien
5	1813	99.1	352	1	CXCR4_PAPAN	P56491 papio anubi
6	1809	98.9	352	2	Q8HZU0_SAISC	Q8hzu0 saimiri sci
7	1806	98.7	352	1	CXCR4_MACFA	Q28474 macaca fasc
8	1806	98.7	352	2	O77488_CERAE	O77488 cercopithec
9	1805	98.6	352	2	Q8HZU1_CALJA	Q8hzu1 callithrix
10	1803	98.5	352	1	CXCR4_MACMU	P79394 macaca mula
11	1803	98.5	352	2	Q9TSQ8_CERAE	Q9tsq8 cercopithec
12	1802	98.5	347	2	Q9MZN2_PONPY	Q9mzn2 pongo pygma
13	1802	98.5	347	2	Q9MZN1_9PRIM	Q9mzn1 gorilla gor
14	1802	98.5	347	2	Q9MZN6_HYLLE	Q9mzn6 nomascus le

15	1802	98.5	347	2	Q9MZN5_BUNHO	Q9mzn5 bunopithecu
16	1799	98.3	352	2	Q9BDS5_MACFA	Q9bds5 macaca fasc
17	1798	98.3	347	2	Q9MZN4_HYLLA	Q9mzn4 hylobates l
18	1798	98.3	352	2	Q7YS92_9EUTH	Q7ys92 tupaia chin
19	1795	98.1	352	1	CXCR4_CERTO	O62747 cercocebus
20	1792	97.9	347	2	Q9MZN3_HYLSY	Q9mzn3 hylobates s
21	1786	97.6	347	2	Q9MZP5_9PRIM	Q9mzp5 presbytis p
22	1786	97.6	347	2	Q9MZP8_COLPO	Q9mzp8 colobus pol
23	1786	97.6	347	2	Q9MZQ2_PYGRO	Q9mzq2 pygathrix r
24	1786	97.6	347	2	Q9MZQ1_PYGBI	Q9mzq1 pygathrix b
25	1786	97.6	347	2	Q9MZP0_MACAS	Q9mzp0 macaca assa
26	1786	97.6	347	2	Q9MZN8_MACTH	Q9mzn8 macaca thib
27	1786	97.6	347	2	Q9MZN7_MACNE	Q9mzn7 macaca neme
28	1786	97.6	347	2	Q9MZP9_NASLA	Q9mzp9 nasalis lar
29	1786	97.6	347	2	Q9MZQ3_PYGAV	Q9mzq3 pygathrix a
30	1786	97.6	347	2	Q9MZQ0_PYGNE	Q9mzq0 pygathrix n
31	1786	97.6	347	2	Q9MZP4_PREFR	Q9mzp4 presbytis f
32	1786	97.6	347	2	Q9MZN9_MACAR	Q9mzn9 macaca arct
33	1782	97.4	347	2	Q9MZP7_9PRIM	Q9mzp7 presbytis s
34	1782	97.4	347	2	Q9MZP2_MANSP	Q9mzp2 mandrillus
35	1781	97.3	347	2	Q9MZM9_ATEPA	Q9mzm9 ateles pani
36	1779	97.2	347	2	Q9MZM5_PITPI	Q9mzm5 pithecia pi
37	1779	97.2	347	2	Q9MZM7_CALGO	Q9mzm7 callimico g
38	1778	97.2	347	2	Q9MZP6_9PRIM	Q9mzp6 presbytis j
39	1778	97.2	347	2	Q9MZP3_SEMEN	Q9mzp3 semnopithec
40	1777	97.1	347	2	Q9MZN0_ALOSE	Q9mzn0 alouatta se
41	1771	96.8	347	2	Q9MZP1_MANLE	Q9mzp1 mandrillus
42	1771	96.8	347	2	Q9MZM6_CALMO	Q9mzm6 callicebus
43	1760	96.2	347	2	Q9MZM8_CALJA	Q9mzm8 callithrix
44	1754.5	95.9	353	2	Q3LSL6_CANFA	Q3lsl6 canis famil
45	1754	95.8	347	2	Q9MZM1_EULMA	Q9mzm1 eulemur mac

ALIGNMENTS

```
RESULT 1
CXCR4_HUMAN
ID   CXCR4_HUMAN     STANDARD;      PRT;   352 AA.
AC   P61073; O60835; P30991; P56438; Q9UKN2;
DT   26-APR-2004, integrated into UniProtKB/Swiss-Prot.
DT   26-APR-2004, sequence version 1.
DT   13-JUN-2006, entry version 27.
DE   C-X-C chemokine receptor type 4 (CXC-R4) (CXCR-4) (Stromal cell-
DE   derived factor 1 receptor) (SDF-1 receptor) (Fusin) (Leukocyte-derived
DE   seven transmembrane domain receptor) (LESTR) (LCR1) (FB22) (NPYRL)
DE   (HM89) (CD184 antigen).
GN   Name=CXCR4;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND FUNCTION.
RC   TISSUE=Lung;
RX   MEDLINE=93319629; PubMed=8329116;
RA   Herzog H., Hort Y.J., Shine J., Selbie L.A.;
RT   "Molecular cloning, characterization, and localization of the human
RT   homolog to the reported bovine NPY Y3 receptor: lack of NPY binding
RT   and activation.";
RL   DNA Cell Biol. 12:465-471(1993).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND FUNCTION.
RC   TISSUE=Fetal brain;
RX   MEDLINE=94052833; PubMed=8234909; DOI=10.1016/0167-0115(93)90392-L;
RA   Jazin E.E., Yoo H., Blomqvist A.G., Yee F., Weng G., Walker M.W.,
RA   Salon J., Larhammar D., Wahlestedt C.R.;
RT   "A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its
RT   human homologue, confers neither NPY binding sites nor NPY
RT   responsiveness on transfected cells.";
RL   Regul. Pept. 47:247-258(1993).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RC   TISSUE=Fetal spleen;
RX   MEDLINE=93315164; PubMed=8325644;
```

RA Federsppiel B., Melhado I.G., Duncan A.M., Delaney A.D.,
RA Schappert K.T., Clark-Lewis I., Jirik F.R.;
RT "Molecular cloning of the cDNA and chromosomal localization of the
RT gene for a putative seven-transmembrane segment (7-TMS) receptor
RT isolated from human spleen.";
RL Genomics 16:707-712(1993).
RN [4]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RC TISSUE=Monocyte;
RX MEDLINE=94103215; PubMed=8276799;
RA Loetscher M., Geiser T., O'Reilly T., Zwahlen R., Baggiolini M.,
RA Moser B.;
RT "Cloning of a human seven-transmembrane domain receptor, LESTR, that
RT is highly expressed in leukocytes.";
RL J. Biol. Chem. 269:232-237(1994).
RN [5]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RX MEDLINE=94092629; PubMed=7505609;
RA Nomura H., Nielsen B.W., Matsushima K.;
RT "Molecular cloning of cDNAs encoding a LD78 receptor and putative
RT leukocyte chemotactic peptide receptors.";
RL Int. Immunol. 5:1239-1249(1993).
RN [6]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND CHARACTERIZATION OF ITS
RP HIV-1 CORECEPTOR FUNCTION.
RX MEDLINE=96217947; PubMed=8629022;
RA Feng Y., Broder C.C., Kennedy P.E., Berger E.A.;
RT "HIV-1 entry cofactor: functional cDNA cloning of a seven-
RT transmembrane, G protein-coupled receptor.";
RL Science 272:872-877(1996).
RN [7]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC TISSUE=Peripheral blood leukocyte;
RX MEDLINE=98136183; PubMed=9468539; DOI=10.1074/jbc.273.8.4754;
RA Wegner S.A., Ehrenberg P.K., Chang G., Dayhoff D.E., Sleeker A.L.,
RA Michael N.L.;
RT "Genomic organization and functional characterization of the chemokine
RT receptor CXCR4, a major entry co-receptor for human immunodeficiency
RT virus type 1.";
RL J. Biol. Chem. 273:4754-4760(1998).
RN [8]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=98258970; PubMed=9599023; DOI=10.1016/S0014-5793(98)00359-7;
RA Caruz A., Samsom M., Alonso J.M., Alcami J., Baleux F.,
RA Virelizier J.-L., Parmentier M., Arenzana-Seisdedos F.;
RT "Genomic organization and promoter characterization of human CXCR4
RT gene.";
RL FEBS Lett. 426:271-278(1998).
RN [9]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RX MEDLINE=99408510; PubMed=10480633; DOI=10.1089/088922299310296;
RA Xiao L., Weiss S.H., Qari S.H., Rudolph D., Zhao C., Denny T.N.,
RA Hodge T., Lal R.B.;
RT "Partial resistance to infection by R5X4 primary HIV type 1 isolates
RT in an exposed-uninfected individual homozygous for CCR5 32-base pair
RT deletion.";
RL AIDS Res. Hum. Retroviruses 15:1201-1208(1999).
RN [10]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC TISSUE=Peripheral blood lymphocyte;
RX MEDLINE=99095114; PubMed=9879064;
RA Frodl R., Gierschik P., Moepps B.;
RT "Genomic organization and expression of the CXCR4 gene in mouse and
RT man: absence of a splice variant corresponding to mouse CXCR4-B in
RT human tissues.";
RL J. Recept. Signal Transduct. Res. 18:321-344(1998).
RN [11]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2).
RC TISSUE=Neutrophil;
RX MEDLINE=99384048; PubMed=10452968;
RA Gupta S.K., Pillarisetti K.;
RT "CXCR4-Lo: molecular cloning and functional expression of a novel
RT human CXCR4 splice variant.";
RL J. Immunol. 163:2368-2372(1999).
RN [12]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).

RC TISSUE=Lung;
RA Warren C.N., Aronstam R.S., Sharma S.V.;
RT "cDNA clones of human proteins involved in signal transduction
RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
RN [13]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,
RA Rajkumar N., Yi Q., Nickerson D.A.;
RT "SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-
RT FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
RN [14]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RA Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDSs in BD Creator(TM) system donor
RT vector.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
RN [15]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [16]
RP SULFATION.
RX MEDLINE=99189752; PubMed=10089882; DOI=10.1016/S0092-8674(00)80577-2;
RA Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M.,
RA Gerard N.P., Gerard C., Sodroski J., Choe H.;
RT "Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1
RT entry.";
RL Cell 96:667-676(1999).
RN [17]
RP FUNCTION.
RX MEDLINE=96351077; PubMed=8752280; DOI=10.1038/382829a0;
RA Bleul C.C., Farzan M., Choe H., Parolin C., Clark-Lewis I.,
RA Sodroski J., Springer T.A.;
RT "The lymphocyte chemoattractant SDF-1 is a ligand for LESTR/fusin and
RT blocks HIV-1 entry.";
RL Nature 382:829-833(1996).
RN [18]
RP FUNCTION.
RX MEDLINE=96351078; PubMed=8752281; DOI=10.1038/382833a0;
RA Oberlin E., Amara A., Bachelerie F., Bessia C., Virelizier J.-L.,
RA Arenzana-Seisdedos F., Schwartz O., Heard J.-M., Clark-Lewis I.,
RA Legler D.F., Loetscher M., Baggiolini M., Moser B.;
RT "The CXC chemokine SDF-1 is the ligand for LESTR/fusin and prevents
RT infection by T-cell-line-adapted HIV-1.";
RL Nature 382:833-835(1996).
RN [19]
RP ERRATUM.
RA Oberlin E., Amara A., Bachelerie F., Bessia C., Virelizier J.-L.,
RA Arenzana-Seisdedos F., Schwartz O., Heard J.-M., Clark-Lewis I.,
RA Legler D.F., Loetscher M., Baggiolini M., Moser B.;
RL Nature 384:288-288(1996).
RN [20]

```
RP   CHARACTERIZATION AS HIV-1 CORECEPTOR.
RX   MEDLINE=97002453; PubMed=8849450; DOI=10.1126/science.274.5287.602;
RA   Lapham C.K., Ouyang J., Chandrasekhar B., Nguyen N.Y., Dimitrov D.S.,
RA   Golding H.;
RT   "Evidence for cell-surface association between fusin and the CD4-gp120
RT   complex in human cell lines.";
RL   Science 274:602-605(1996).
RN   [21]
RP   CHARACTERIZATION AS HIV-2 PRIMARY RECEPTOR IN SOME ISOLATES.
RX   MEDLINE=97083584; PubMed=8929542; DOI=10.1016/S0092-8674(00)81393-8;
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Query Match 100.0%; Score 1830; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.5e-133;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
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RESULT 2
CXCR4_PANTR
ID   CXCR4_PANTR    STANDARD;      PRT;   352 AA.
AC   P61072; O60835; P30991; P56438; Q9UKN2;
DT   26-APR-2004, integrated into UniProtKB/Swiss-Prot.
DT   26-APR-2004, sequence version 1.
DT   18-APR-2006, entry version 19.
DE   C-X-C chemokine receptor type 4 (CXC-R4) (CXCR-4) (SDF-1 receptor)
DE   (Stromal cell-derived factor 1 receptor) (Fusin) (CD184 antigen).
GN   Name=CXCR4;
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=98090115; PubMed=9430250;
RA   Pretet J.-L., Zerbib A.C., Girard M., Guillet J.-G., Butor C.;
RT   "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1.";
RL   AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
CC   -!- FUNCTION: Receptor for the C-X-C chemokine CXCL12/SDF-1.
CC       Transduces a signal by increasing the intracellular calcium ions
CC       level (By similarity).
CC   -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
CC   -!- PTM: Sulfated (By similarity).
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; U89798; AAC03718.1; -; mRNA.
DR   InterPro; IPR000355; Chmkine_rcpt.
DR   InterPro; IPR001277; CXC_4_rcpt.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
```

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DR   PRINTS; PR00657; CCCHEMOKINER.
DR   PRINTS; PR00645; CXCCHMKINER4.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Membrane; Receptor;
KW   Sulfation; Transducer; Transmembrane.
FT   CHAIN         1    352       C-X-C chemokine receptor type 4.
FT                                /FTId=PRO_0000069356.
FT   TOPO_DOM      1     39       Extracellular (Potential).
FT   TRANSMEM     40     63       1 (Potential).
FT   TOPO_DOM     64     79       Cytoplasmic (Potential).
FT   TRANSMEM     80     99       2 (Potential).
FT   TOPO_DOM    100    110       Extracellular (Potential).
FT   TRANSMEM    111    132       3 (Potential).
FT   TOPO_DOM    133    154       Cytoplasmic (Potential).
FT   TRANSMEM    155    175       4 (Potential).
FT   TOPO_DOM    176    200       Extracellular (Potential).
FT   TRANSMEM    201    220       5 (Potential).
FT   TOPO_DOM    221    240       Cytoplasmic (Potential).
FT   TRANSMEM    241    261       6 (Potential).
FT   TOPO_DOM    262    285       Extracellular (Potential).
FT   TRANSMEM    286    305       7 (Potential).
FT   TOPO_DOM    306    352       Cytoplasmic (Potential).
FT   MOD_RES      21     21       Sulfotyrosine (Potential).
FT   CARBOHYD     11     11       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    109    186       By similarity.
SQ   SEQUENCE   352 AA;  39746 MW;  8C8476A186786B83 CRC64;

  Query Match             100.0%;  Score 1830;  DB 1;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-133;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 3
Q53S69_HUMAN
ID   Q53S69_HUMAN   PRELIMINARY;   PRT;   352 AA.
AC   Q53S69;
DT   24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   24-MAY-2005, sequence version 1.
DT   13-JUN-2006, entry version 13.
DE   Hypothetical protein CXCR4.
GN   Name=CXCR4;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Abbott A., Lamar B., Ureta M.;
RT   "The sequence of Homo sapiens BAC clone RP11-809C23.";
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RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Waterston R.H.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Waterston R.;
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RA   Wilson R.K.;
RL   Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Membrane (By similarity).
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AC068492; AAY24044.1; -; Genomic_DNA.
DR   UniGene; Hs.421986; -.
DR   Ensembl; ENSG00000121966; Homo sapiens.
DR   RZPD-ProtExp; A0419; -.
DR   RZPD-ProtExp; RZPDo834F0245; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR   GO; GO:0016494; F:C-X-C chemokine receptor activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR000355; Chmkine_rcpt.
DR   InterPro; IPR001277; CXC_4_rcpt.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00657; CCCHEMOKINER.
DR   PRINTS; PR00645; CXCCHMKINER4.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Hypothetical protein; Membrane; Receptor;
KW   Transducer; Transmembrane.
SQ   SEQUENCE   352 AA;  39746 MW;  8C8476A186786B83 CRC64;

  Query Match             100.0%;  Score 1830;  DB 2;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-133;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 4
Q9BXA0_HUMAN
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ID   Q9BXA0_HUMAN   PRELIMINARY;   PRT;   352 AA.
AC   Q9BXA0;
DT   01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2001, sequence version 1.
DT   13-JUN-2006, entry version 25.
DE   Chemokine receptor CXCR4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Fan Z., Li T., Li J., Luo B.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Membrane (By similarity).
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AF348491; AAK29630.1; -; mRNA.
DR   Ensembl; ENSG00000121966; Homo sapiens.
DR   RZPD-ProtExp; A0419; -.
DR   RZPD-ProtExp; RZPDo834F0245; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR   GO; GO:0016494; F:C-X-C chemokine receptor activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR000355; Chmkine_rcpt.
DR   InterPro; IPR001277; CXC_4_rcpt.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00657; CCCHEMOKINER.
DR   PRINTS; PR00645; CXCCHMKINER4.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Membrane; Receptor; Transducer;
KW   Transmembrane.
SQ   SEQUENCE   352 AA;  39743 MW;  0A5F0E4210C81469 CRC64;

  Query Match            99.6%;  Score 1822;  DB 2;  Length 352;
  Best Local Similarity  99.4%;  Pred. No. 2.7e-132;
  Matches  350;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              |:| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TIIPILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352

RESULT 5
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CXCR4_PAPAN
ID   CXCR4_PAPAN     STANDARD;      PRT;   352 AA.
AC   P56491;
DT   15-JUL-1998, integrated into UniProtKB/Swiss-Prot.
DT   15-JUL-1998, sequence version 1.
DT   18-APR-2006, entry version 33.
DE   C-X-C chemokine receptor type 4 (CXC-R4) (CXCR-4) (SDF-1 receptor)
DE   (Stromal cell-derived factor 1 receptor) (Fusin) (CD184 antigen).
GN   Name=CXCR4;
OS   Papio anubis (Olive baboon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Catarrhini; Cercopithecidae; Cercopithecinae; Papio.
OX   NCBI_TaxID=9555;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=98346785; PubMed=9683255; DOI=10.1016/S0161-5890(98)00016-9;
RA   Benton P.A., Lee D.R., Kennedy R.C.;
RT   "Sequence comparisons of non-human primate HIV-1 coreceptor
RT   homologues.";
RL   Mol. Immunol. 35:95-101(1998).
CC   -!- FUNCTION: Receptor for the C-X-C chemokine CXCL12/SDF-1.
CC       Transduces a signal by increasing the intracellular calcium ions
CC       level (By similarity).
CC   -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
CC   -!- PTM: Sulfated (By similarity).
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AF031089; AAC63831.1; -; mRNA.
DR   InterPro; IPR000355; Chmkine_rcpt.
DR   InterPro; IPR001277; CXC_4_rcpt.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00657; CCCHEMOKINER.
DR   PRINTS; PR00645; CXCCHMKINER4.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Membrane; Receptor;
KW   Sulfation; Transducer; Transmembrane.
FT   CHAIN         1    352       C-X-C chemokine receptor type 4.
FT                                /FTId=PRO_0000069357.
FT   TOPO_DOM      1     39       Extracellular (Potential).
FT   TRANSMEM     40     63       1 (Potential).
FT   TOPO_DOM     64     79       Cytoplasmic (Potential).
FT   TRANSMEM     80     99       2 (Potential).
FT   TOPO_DOM    100    110       Extracellular (Potential).
FT   TRANSMEM    111    132       3 (Potential).
FT   TOPO_DOM    133    154       Cytoplasmic (Potential).
FT   TRANSMEM    155    175       4 (Potential).
FT   TOPO_DOM    176    200       Extracellular (Potential).
FT   TRANSMEM    201    220       5 (Potential).
FT   TOPO_DOM    221    240       Cytoplasmic (Potential).
FT   TRANSMEM    241    261       6 (Potential).
FT   TOPO_DOM    262    285       Extracellular (Potential).
FT   TRANSMEM    286    305       7 (Potential).
FT   TOPO_DOM    306    352       Cytoplasmic (Potential).
FT   MOD_RES      21     21       Sulfotyrosine (Potential).
FT   CARBOHYD     11     11       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    109    186       By similarity.
SQ   SEQUENCE   352 AA;  39752 MW;  468E542E1851265A CRC64;

  Query Match             99.1%;  Score 1813;  DB 1;  Length 352;
  Best Local Similarity   98.9%;  Pred. No. 1.3e-131;
  Matches  348;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||:||||||||||:||:||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSIKEPCFREENAHFNRIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
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Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFASVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 6
Q8HZU0_SAISC
ID   Q8HZU0_SAISC   PRELIMINARY;   PRT;   352 AA.
AC   Q8HZU0;
DT   01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2003, sequence version 1.
DT   30-MAY-2006, entry version 19.
DE   Chemokine receptor CXCR4.
OS   Saimiri sciureus (Common squirrel monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Platyrrhini; Cebidae; Saimiriinae; Saimiri.
OX   NCBI_TaxID=9521;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22174698; PubMed=12186836; DOI=10.1084/jem.20020468;
RA   LaBonte J.A., Babcock G.J., Patel T., Sodroski J.;
RT   "Blockade of HIV-1 infection of New World monkey cells occurs
RT   primarily at the stage of virus entry.";
RL   J. Exp. Med. 196:431-445(2002).
CC   -!- SUBCELLULAR LOCATION: Membrane (By similarity).
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AF452613; AAN14529.1; -; mRNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR   GO; GO:0016494; F:C-X-C chemokine receptor activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR000355; Chmkine_rcpt.
DR   InterPro; IPR001277; CXC_4_rcpt.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00657; CCCHEMOKINER.
DR   PRINTS; PR00645; CXCCHMKINER4.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Membrane; Receptor; Transducer;
KW   Transmembrane.
SQ   SEQUENCE   352 AA;  39821 MW;  BF1A21FB0C8D4487 CRC64;

  Query Match             98.9%;  Score 1809;  DB 2;  Length 352;
  Best Local Similarity   98.6%;  Pred. No. 2.7e-131;
  Matches  347;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||:||||||||||:||:||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSIKEPCFREENAHFNRIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
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Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGKFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIRQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 7
CXCR4_MACFA
ID   CXCR4_MACFA    STANDARD;      PRT;   352 AA.
AC   Q28474;
DT   15-JUL-1998, integrated into UniProtKB/Swiss-Prot.
DT   01-NOV-1996, sequence version 1.
DT   18-APR-2006, entry version 35.
DE   C-X-C chemokine receptor type 4 (CXC-R4) (CXCR-4) (SDF-1 receptor)
DE   (Stromal cell-derived factor 1 receptor) (Fusin) (LESTR) (CD184
DE   antigen).
GN   Name=CXCR4;
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RA   Tatsumi M., Takahashi H.;
RT   "Monkey CD4 and fusin are not species barrier for HIV-1 replication.";
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor for the C-X-C chemokine CXCL12/SDF-1.
CC       Transduces a signal by increasing the intracellular calcium ions
CC       level (By similarity).
CC   -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
CC   -!- PTM: Sulfated (By similarity).
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; D86579; BAA13126.1; -; mRNA.
DR   PIR; G00048; G00048.
DR   InterPro; IPR000355; Chmkine_rcpt.
DR   InterPro; IPR001277; CXC_4_rcpt.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00657; CCCHEMOKINER.
DR   PRINTS; PR00645; CXCCHMKINER4.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Membrane; Receptor;
KW   Sulfation; Transducer; Transmembrane.
FT   CHAIN         1    352       C-X-C chemokine receptor type 4.
FT                                /FTId=PRO_0000069353.
FT   TOPO_DOM      1     39       Extracellular (Potential).
FT   TRANSMEM     40     63       1 (Potential).
FT   TOPO_DOM     64     79       Cytoplasmic (Potential).
FT   TRANSMEM     80     99       2 (Potential).
FT   TOPO_DOM    100    110       Extracellular (Potential).
FT   TRANSMEM    111    132       3 (Potential).
FT   TOPO_DOM    133    154       Cytoplasmic (Potential).
FT   TRANSMEM    155    175       4 (Potential).
FT   TOPO_DOM    176    200       Extracellular (Potential).
FT   TRANSMEM    201    220       5 (Potential).
FT   TOPO_DOM    221    240       Cytoplasmic (Potential).
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FT   TRANSMEM    241    261       6 (Potential).
FT   TOPO_DOM    262    285       Extracellular (Potential).
FT   TRANSMEM    286    305       7 (Potential).
FT   TOPO_DOM    306    352       Cytoplasmic (Potential).
FT   MOD_RES      21     21       Sulfotyrosine (Potential).
FT   CARBOHYD     11     11       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    109    186       By similarity.
SQ   SEQUENCE   352 AA;  39753 MW;  432DA6C11859EF8A CRC64;

  Query Match             98.7%;  Score 1806;  DB 1;  Length 352;
  Best Local Similarity   98.3%;  Pred. No. 4.6e-131;
  Matches  346;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||:||||||||||:||:||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSIKEPCFREENAHFNRIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||:||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLYVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFASVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALGFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 8
O77488_CERAE
ID   O77488_CERAE   PRELIMINARY;   PRT;   352 AA.
AC   O77488;
DT   01-NOV-1998, integrated into UniProtKB/TrEMBL.
DT   01-NOV-1998, sequence version 1.
DT   30-MAY-2006, entry version 31.
DE   CXCR4 receptor.
OS   Cercopithecus aethiops (Green monkey) (Grivet).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Catarrhini; Cercopithecidae; Cercopithecinae; Cercopithecus.
OX   NCBI_TaxID=9534;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Murayama Y., Matsunaga S., Inoue-Murayama M.;
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Membrane (By similarity).
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB015943; BAA31327.1; -; mRNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR   GO; GO:0016494; F:C-X-C chemokine receptor activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR000355; Chmkine_rcpt.
DR   InterPro; IPR001277; CXC_4_rcpt.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00657; CCCHEMOKINER.
DR   PRINTS; PR00645; CXCCHMKINER4.
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DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Membrane; Receptor; Transducer;
KW   Transmembrane.
SQ   SEQUENCE   352 AA;  39774 MW;  DDC9182E14540BE9 CRC64;

  Query Match             98.7%;  Score 1806;  DB 2;  Length 352;
  Best Local Similarity   98.6%;  Pred. No. 4.6e-131;
  Matches  347;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||:||||||||||:||:||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSIKEPCFREENAHFNRIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||:||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPHFIFASVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 9
Q8HZU1_CALJA
ID   Q8HZU1_CALJA   PRELIMINARY;   PRT;   352 AA.
AC   Q8HZU1;
DT   01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2003, sequence version 1.
DT   30-MAY-2006, entry version 19.
DE   Chemokine receptor CXCR4.
OS   Callithrix jacchus (Common marmoset).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Platyrrhini; Cebidae; Callitrichinae; Callithrix.
OX   NCBI_TaxID=9483;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22174698; PubMed=12186836; DOI=10.1084/jem.20020468;
RA   LaBonte J.A., Babcock G.J., Patel T., Sodroski J.;
RT   "Blockade of HIV-1 infection of New World monkey cells occurs
RT   primarily at the stage of virus entry.";
RL   J. Exp. Med. 196:431-445(2002).
CC   -!- SUBCELLULAR LOCATION: Membrane (By similarity).
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AF452612; AAN14528.1; -; mRNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR   GO; GO:0016494; F:C-X-C chemokine receptor activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR000355; Chmkine_rcpt.
DR   InterPro; IPR001277; CXC_4_rcpt.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00657; CCCHEMOKINER.
```

```
DR   PRINTS; PR00645; CXCCHMKINER4.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Membrane; Receptor; Transducer;
KW   Transmembrane.
SQ   SEQUENCE   352 AA;  39803 MW;  8018A4500FC887C0 CRC64;

  Query Match             98.6%;  Score 1805;  DB 2;  Length 352;
  Best Local Similarity   98.3%;  Pred. No. 5.5e-131;
  Matches  346;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||:|||||||:||||||||||:||:||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEIGSGDYDSIKEPCFREENAHFNRIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGKFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIRQGCEFENTVHKWISITEALAFFHCCLNPI 300
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start | next page

SCORE 1.3 BuildDate: 11/17/2006

SCORE Search Results Details f

This page gives you Search Results detail for the Application 10785230 and Search Result 2007020
start

GenCore version 6.2

OM protein - protein search, using sw model

Run on: February 6, 2007, 14:15:46 ; Search time 26 Seconds
(without alignments)
1315.579 Million cell updates/sec

Title: US-10-785-230-1
Perfect score: 1830
Sequence: 1 MEGISIYTSDNYTEEMGSGD.....KRGGHSSVSTESESSSFHSS 352

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1830	100.0	352	2	A45747	neuropeptide Y/pep
2	1806	98.7	352	2	G00048	fusin (LESTRA) - c
3	1722.5	94.1	353	2	S28787	neuropeptide Y/pep
4	600.5	32.8	360	2	A57160	chemokine (C-C) re
5	582	31.8	367	2	JE0349	interferon-inducib
6	568	31.0	360	2	A53611	interleukin-8 rece
7	567	31.0	356	2	S42096	interleukin-8 rece
8	564.5	30.8	360	2	JC4587	chemokine (C-C) re
9	564	30.8	355	2	JQ1231	interleukin-8 rece
10	563	30.8	378	2	A55735	G protein-coupled
11	559.5	30.6	350	2	A39445	interleukin-8 rece
12	558	30.5	358	2	A53752	interleukin-8 rece
13	557	30.4	378	2	B55735	lymphocyte-specifi
14	549.5	30.0	355	2	JC4304	orphan G protein-c
15	544	29.7	327	2	S56162	MDCR15 protein - h
16	540	29.5	372	2	S26667	G protein-coupled
17	539	29.5	359	2	A48921	interleukin-8 rece
18	538	29.4	378	2	A45680	G protein-coupled
19	536	29.3	374	2	S42628	G protein-coupled

20	533.5	29.2	369	2	JC5068	G protein-coupled
21	529	28.9	374	2	S32785	G protein-coupled
22	528	28.9	374	2	I38450	chemokine (C-C) re
23	527	28.8	355	2	JC5067	G protein-coupled
24	519.5	28.4	383	2	S55594	G protein-coupled
25	514.5	28.1	354	2	I58186	probable G protein
26	512.5	28.0	360	2	JC2443	chemokine (C-C) re
27	509	27.8	355	2	G02436	chemokine (C-C) re
28	506	27.7	352	2	A43113	chemokine (C-C) re
29	503.5	27.5	355	2	A45177	chemokine (C-C) re
30	502.5	27.5	359	2	S15403	angiotensin II rec
31	501.5	27.4	350	2	JN0621	G protein-coupled
32	493.5	27.0	359	2	JC1104	angiotensin II rec
33	493.5	27.0	359	2	A42656	angiotensin II rec
34	488.5	26.7	359	2	S44425	angiotensin II rec
35	487.5	26.6	359	2	JQ1516	angiotensin II rec
36	485	26.5	362	2	JN0694	angiotensin II rec
37	484.5	26.5	359	2	A48857	angiotensin II rec
38	483.5	26.4	359	2	JH0621	angiotensin II rec
39	481	26.3	359	2	I49341	MIP-1 alpha recept
40	480.5	26.3	359	2	JC2134	angiotensin II rec
41	474.5	25.9	359	2	I39418	angiotensin II rec
42	473.5	25.9	362	2	A30341	G protein-coupled
43	472.5	25.8	359	2	JC1194	angiotensin II rec
44	469.5	25.7	355	2	I49339	macrophage inflamm
45	469.5	25.7	362	2	A39714	G protein-coupled

ALIGNMENTS

RESULT 1
A45747
neuropeptide Y/peptide YY receptor Y3 - human
N;Alternate names: fusin; HM89; leukocyte-derived seven-transmembrane receptor LESTR; receptor D2S201E
C;Species: Homo sapiens (man)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: A45747; A53103; I53006; I59444; I69203; S32761
R;Federsppiel, B.; Melhado, I.G.; Duncan, A.M.V.; Delaney, A.; Schappert, K.; Clark-Lewis, I.; Jirik, F.R.
Genomics 16, 707-712, 1993
A;Title: Molecular cloning of the cDNA and chromosomal localization of the gene for a putative seven-transm
A;Reference number: A45747; MUID:93315164; PMID:8325644
A;Accession: A45747
A;Molecule type: mRNA
A;Residues: 1-352 <FED>
A;Cross-references: UNIPROT:P61073; UNIPARC:UPI000000106C; GB:M99293; NID:g292516; PIDN:AAA16617.1; PID:g29
R;Loetscher, M.; Geiser, T.; O'Reilly, T.; Zwahlen, R.; Baggiolini, M.; Moser, B.
J. Biol. Chem. 269, 232-237, 1994
A;Title: Cloning of a human seven-transmembrane domain receptor, LESTR, that is highly expressed in leukocy
A;Reference number: A53103; MUID:94103215; PMID:8276799
A;Accession: A53103
A;Molecule type: mRNA
A;Residues: 1-352 <LOE>
A;Cross-references: UNIPARC:UPI000000106C; EMBL:X71635; NID:g297099; PIDN:CAA50641.1; PID:g297100
R;Herzog, H.; Hort, Y.J.; Shine, J.; Selbie, L.A.
DNA Cell Biol. 12, 465-471, 1993
A;Title: Molecular cloning, characterization, and localization of the human homolog to the reported bovine
A;Reference number: I53006; MUID:93319629; PMID:8329116
A;Accession: I53006
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-352 <HER>
A;Cross-references: UNIPARC:UPI000000106C; GB:L06797; NID:g414929; PIDN:AAA03209.1; PID:g414928
R;Jazin, E.E.; Yoo, H.; Blomqvist, A.G.; Yee, F.; Weng, G.; Walker, M.W.; Salon, J.; Larhammar, D.; Wahlest
Regul. Pept. 47, 247-258, 1993
A;Title: A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its human homologue, confers neithe
A;Reference number: I59444; MUID:94052833; PMID:8234909
A;Accession: I59444
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-352 <RE2>
A;Cross-references: UNIPARC:UPI000000106C; GB:L01639; NID:g189313; PIDN:AAA16594.1; PID:g189314
R;Nomura, H.; Nielsen, B.W.; Matsushima, K.
Int. Immunol. 5, 1239-1249, 1993
A;Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte chemotactic peptide rec
A;Reference number: I54751; MUID:94092629; PMID:7505609

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A;Accession: I69203
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-352 <RES>
A;Cross-references: UNIPARC:UPI000000106C; GB:D10924; NID:g219868; PIDN:BAA01722.1; PID:g219869
C;Genetics:
A;Gene: GDB:NPY3R; NPYY3
A;Cross-references: GDB:230002; OMIM:162643
A;Map position: 2q21-2q21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

  Query Match             100.0%;  Score 1830;  DB 2;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-148;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 2
G00048
fusin (LESTRA) - crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
C;Accession: G00048
R;Tatsumi, M.
submitted to GenBank, July 1996
A;Reference number: H00048
A;Accession: G00048
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-352 <TAT>
A;Cross-references: UNIPROT:Q28474; UNIPARC:UPI0000127302; GB:D86579; NID:g1468948; PID:g1468949
C;Superfamily: vertebrate rhodopsin

  Query Match             98.7%;  Score 1806;  DB 2;  Length 352;
  Best Local Similarity   98.3%;  Pred. No. 3.6e-146;
  Matches  346;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||:||||||||||:||:||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSIKEPCFREENAHFNRIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLYVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFASVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
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Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALGFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 3
S28787
neuropeptide Y/peptide YY receptor Y3 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: S28787
R;Rimland, J.; Xin, W.; Sweetnam, P.; Saijoh, K.; Nestler, E.J.; Duman, R.S.
Mol. Pharmacol. 40, 869-875, 1991
A;Title: Sequence and expression of a neuropeptide Y receptor cDNA.
A;Reference number: S28787; MUID:92100053; PMID:1661837
A;Accession: S28787
A;Molecule type: mRNA
A;Residues: 1-353 <RIM>
A;Cross-references: UNIPROT:P25930; UNIPARC:UPI00001272FF; EMBL:M86739
C;Superfamily: vertebrate rhodopsin
C;Keywords: appetite; G protein-coupled receptor; transmembrane protein

  Query Match             94.1%;  Score 1722.5;  DB 2;  Length 353;
  Best Local Similarity   92.4%;  Pred. No. 4.6e-139;
  Matches  326;  Conservative   20;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 MEGISIYTSDNYTE-EMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLV 59
              |||| |:|||||||| ::|||||||||||||||||:||:|||||:||||||||||||||
Db          1 MEGIRIFTSDNYTEDDLGSGDYDSMKEPCFREENAHFNRIFLPTVYSIIFLTGIVGNGLV 60

Qy         60 ILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVN 119
              ||||||||||||||||||||||||||||:|||||||||||||||| ||||||||||||
Db         61 ILVMGYQKKLRSMTDKYRLHLSVADLLFVLTLPFWAVDAVANWYFGKFLCKAVHVIYTVN 120

Qy        120 LYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSE 179
              ||||||||||||||||||||||||||:|||||||||||||||:||:|||||| |||:: |
Db        121 LYSSVLILAFISLDRYLAIVHATNSQKPRKLLAEKVVYVGVWLPAVLLTIPDLIFADIKE 180

Qy        180 ADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALK 239
               |:|||||||||:|||:||||||||:|||:|||||||||||||||||||:|||||||
Db        181 VDERYICDRFYPSDLWLVVFQFQHIVVGLLLPGIVILSCYCIIISKLSHSKGYQKRKALK 240

Qy        240 TTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNP 299
              ||||||| |||||||||||||||||||||:|||||:||||||||||||||||||||||
Db        241 TTVILILTFFACWLPYYIGISIDSFILLEIIQQGCEFESTVHKWISITEALAFFHCCLNP 300

Qy        300 ILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 353


RESULT 4
A57160
chemokine (C-C) receptor 4 - human
N;Alternate names: C-C CKR-4
C;Species: Homo sapiens (man)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: A57160
R;Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; Wells, T.N.C.
J. Biol. Chem. 270, 19495-19500, 1995
A;Title: Molecular cloning and functional expression of a novel CC chemokine receptor cDNA from a human bas
A;Reference number: A57160; MUID:95370289; PMID:7642634
A;Accession: A57160
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-360 <POW>
A;Cross-references: UNIPROT:P51679; UNIPARC:UPI000002DFE9; GB:X85740; NID:g1370103; PIDN:CAA59743.1; PID:g9
A;Note: source clone K5-5
C;Genetics:
A;Gene: GDB:CMKBR4
A;Cross-references: GDB:677463
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A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F;40-65/Domain: transmembrane #status predicted <TM1>
F;76-97/Domain: transmembrane #status predicted <TM2>
F;112-133/Domain: transmembrane #status predicted <TM3>
F;151-175/Domain: transmembrane #status predicted <TM4>
F;208-226/Domain: transmembrane #status predicted <TM5>
F;243-264/Domain: transmembrane #status predicted <TM6>
F;291-308/Domain: transmembrane #status predicted <TM7>
F;29-276,110-187/Disulfide bonds: #status predicted
F;72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

  Query Match 32.8%; Score 600.5; DB 2; Length 360;
  Best Local Similarity 39.7%; Pred. No. 1.5e-43;
  Matches 116; Conservative 60; Mismatches 113; Indels 3; Gaps 2;

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Qy         21 YDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVMGYQKKLRSMTDKYRLHL 80
              |:|: :|| :|    | ::||| :||::|: |::|| :|:||:   |:||||||  | |:|
Db         22 YESIPKPCTKEGIKAFGELFLPPLYSLVFVFGLLGNSVVVLVLFKYKRLRSMTDVYLLNL 81

Qy         81 SVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSSVLILAFISLDRYLAIVH 140
              :::|||||| :||||   |   | ||  ||| :  :| |  || :  :  :|:|||||||||
Db         82 AISDLLFVFSLPFWGYYAADQWVFGLGLCKMISWMYLVGFYSGIFFVMLMSIDRYLAIVH 141

Qy        141 ATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEADDRYICDRFYP--NDLWVVV 198
              |  | | | |    :  :  |  |:  ::| |:|:      :   |   |   :  | |:
Db        142 AVFSLRARTLTYGVITSLATWSVAVFASLPGFLFSTCYTERNHTYCKTKYSLNSTTWKVL 201

Qy        199 FQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTVILILAFFACWLPYYIG 258
                 :  ::||::|  ::| || :||  | | |  :| ||:|    ::: |   | || |
Db        202 SSLEINILGLVIPLGIMLFCYSMIIRTLQHCKNEKKNKAVKMIFAVVVLFLGFWTPYNIV 261

Qy        259 ISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPILYAFLGAKFK 310
              : ::: : ||:: | | ||  :   |  || ||| |||||||:| ||| ||:
Db        262 LFLETLVELEVL-QDCTFERYLDYAIQATETLAFVHCCLNPIIYFFLGEKFR 312
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RESULT 5
JE0349
interferon-inducible protein 10 (IP-10) receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004
C;Accession: JE0349
R;Tamaru, M.; Tominaga, Y.; Yatsunami, K.; Narumi, S.
Biochem. Biophys. Res. Commun. 251, 41-48, 1998
A;Title: Cloning of the murine interferon-inducible protein 10 (IP-10) receptor and its specific expression
A;Reference number: JE0349; MUID:99009219; PMID:9790904
A;Accession: JE0349
A;Molecule type: mRNA
A;Residues: 1-367 <TAM>
A;Cross-references: UNIPROT:Q9QWN6; UNIPARC:UPI0000029B69; DDBJ:AB003174; NID:g3798731; PIDN:BAA34045.1; PI
C;Comment: This protein is important for lymphocyte trafficking to lymphoid organs.
C;Superfamily: vertebrate rhodopsin

  Query Match 31.8%; Score 582; DB 2; Length 367;
  Best Local Similarity 35.6%; Pred. No. 5.7e-42;
  Matches 121; Conservative 70; Mismatches 133; Indels 16; Gaps 6;

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Qy         15 EMGSGDYD-SMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVMGYQKKLRSMT 73
              : |  : | |   || :: : ||:: ||| :||::|| |::||| |  |:  |:   | |
Db         28 DYGENESDFSDSPPCPQDFSLNFDRTFLPALYSLLFLLGLLGNGAVAAVLLSQRTALSST 87

Qy         74 DKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSSVLILAFISLD 133
              | : |||:|||:| |:||| |||||   | ||  |||    :: :| |:   :|| || |
Db         88 DTFLLHLAVADVLLVLTLPLWAVDAAVQWVFGPGLCKVAGALFNINFYAGAFLLACISFD 147

Qy        134 RYLAIVHATNSQR--PRKLLAEKVVYVGVWIPALLLTIPDFIF--ANVSEADDRYICDRF 189
              |||:|||||   |  ||  :|  :  : ||   ||  :||||:  ||  :  :   |
Db        148 RYLSIVHATQIYRRDPRVRVA--LTCIVVWGLCLLFALPDFIYLSANYDQRLNATHCQYN 205

Qy        190 YPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTVILILAFF 249
              :|  :     :   :: | :|| :|:  ||  |:: |  |:| :: :|::  |::: ||
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Db        206 FP-QVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRFRAMRLVVVVVAAFA 264

Qy        250 ACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPILYAFLGAKF 309
              || ||:: : :|  : : :: : |  |: |    |:|  : : ||||||:||||:| ||
Db        265 VCWTPYHLVVLVDILMDVGVLARNCGRESHVDVAKSVTSGMGYMHCCLNPLLYAFVGVKF 324

Qy        310 KTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSF 349
              :       | : |          :||     |:   ||:
Db        325 REQMWMLFTRLGRSD--------QRGPQRQPSSSRRESSW 356


RESULT 6
A53611
interleukin-8 receptor type B - human
C;Species: Homo sapiens (man)
C;Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: I37898; I38712; A53611; A39446
R;Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
J. Biol. Chem. 269, 26381-26389, 1994
A;Title: Comparison of the genomic organization and promoter function for human interleukin-8 receptors A a
A;Reference number: I37898; MUID:95014476; PMID:7929358
A;Accession: I37898
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-360 <RES>
A;Cross-references: UNIPROT:P25025; UNIPARC:UPI000004358A; EMBL:U11869; NID:g511801; PIDN:AAB60656.1; PID:g
A;Accession: I38712
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-15 <RE2>
A;Cross-references: UNIPARC:UPI000000053D; EMBL:U11872; NID:g511808; PIDN:AAA64380.1; PID:g511809; EMBL:U11
R;Sprenger, H.; Lloyd, A.R.; Lautens, L.L.; Bonner, T.I.; Kelvin, D.J.
J. Biol. Chem. 269, 11065-11072, 1994
A;Title: Structure, genomic organization, and expression of the human interleukin-8 receptor B gene.
A;Reference number: A53611; MUID:94209273; PMID:7512557
A;Accession: A53611
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 6-360 <SPR>
A;Cross-references: UNIPARC:UPI00000746D6; GB:M99412; GB:L19593
R;Murphy, P.M.; Tiffany, H.L.
Science 253, 1280-1283, 1991
A;Title: Cloning of complementary DNA encoding a functional human interleukin-8 receptor.
A;Reference number: A39446; MUID:91368200; PMID:1891716
A;Accession: A39446
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 6-360 <MUR>
A;Cross-references: UNIPARC:UPI00000746D6; GB:M73969
C;Comment: This receptor, unlike IL8RA, binds several peptides besides interleukin-8, including GRO, NAP-2,
C;Genetics:
A;Gene: GDB:IL8RB; IL8RA
A;Cross-references: GDB:127868; OMIM:146928
A;Map position: 2q35-2q35
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

  Query Match             31.0%;  Score 568;  DB 2;  Length 360;
  Best Local Similarity   35.3%;  Pred. No. 8.7e-41;
  Matches  132;  Conservative   69;  Mismatches  119;  Indels   54;  Gaps   11;

Qy          9 SDNYT-----EEMGSGDYDSM-------KEPCFREENANFNKIFLPTIYSIIFLTGIVGN 56
              ||::      |:: :  | |          ||   |:   || |:  ||:::||  ::||
Db          8 SDSFEDFWKGEDLSNYSYSSTLPPFLLDAAPC-EPESLEINKYFVVIIYALVFLLSLLGN 66

Qy         57 GLVILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIY 116
               ||:||: | :  ||:|| | |:|::|||||| :||| ||   |  | || |||| | ::
Db         67 SLVMLVILYSRVGRSVTDVYLLNLALADLLFALTLPIWAASKVNGWIFGTFLCKVVSLLK 126

Qy        117 TVNLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIF-- 174
              || || :|:|| ||:||||||||||| :   :: |  | : : :|  :||| :|  :|
Db        127 EVNFYSGILLLACISVDRYLAIVHATRTLTQKRYLV-KFICLSIWGLSLLLALPVLLFRR 185

Qy        175 ----ANVSEADDRYICDRFYPNDL--WVVVFQFQHIMVGLILPGIVILSCYCIIISKLSH 228
                  :||| |     |     |:   | :: :      | |:| :::| ||   :  |
Db        186 TVYSSNVSPA-----CYEDMGNNTANWRMLLRILPQSFGFIVPLLIMLFCYGFTLRTLFK 240
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Qy        229 SKGHQKRKALKTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITE 288
              :   || :|::    ::| |  ||||| : :  |: :  ::|:: ||  | : : :  ||
Db        241 AHMGQKHRAMRVIFAVVLIFLLCWLPYNLVLLADTLMRTQVIQETCERRNHIDRALDATE 300

Qy        289 ALAFFHCCLNPILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTES---- 344
               |   | ||||::|||:| ||:    | |        ||||:      |  :| :|
Db        301 ILGILHSCLNPLIYAFIGQKFR----HGL--------LKILAI-----HGLISKDSLPKD 343

Qy        345 ------ESSSFHSS 352
                     ||| |:|
Db        344 SRPSFVGSSSGHTS 357


RESULT 7
S42096
interleukin-8 receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-Aug-1999
C;Accession: S42096
R;Gobl, A.E.; Wang, S.; Zhou, Y.; Oeberg, K.
submitted to the EMBL Data Library, February 1994
A;Description: Molecular cloning of the rat IL8 receptor.
A;Reference number: S42096
A;Accession: S42096
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-356 <GOB>
A;Cross-references: UNIPARC:UPI00001778DE; EMBL:X77797
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

  Query Match             31.0%;  Score 567;  DB 2;  Length 356;
  Best Local Similarity   36.3%;  Pred. No. 1e-40;
  Matches  131;  Conservative   68;  Mismatches  126;  Indels   36;  Gaps   11;

Qy         10 DNYT-EEMGSGDYDSMK------------EPCFREENANFNKIFLPTIYSIIFLTGIVGN 56
              ||:: |:  ||| ||               ||    | : |:  :  || :: |  :|||
Db          7 DNFSLEDFFSGDIDSYNFSSDPPFTLSDAAPC-PSANLDINRYAVVVIYVLVTLLSLVGN 65

Qy         57 GLVILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIY 116
               ||:||: | :   |:|| | |:|::||| | :||| ||   |  | ||:|||     :
Db         66 SLVMLVILYNRSTCSVTDVYLLNLAIADLFFALTLPVWAASKVNGWIFGSFLCKVFSFLQ 125

Qy        117 TVNLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFAN 176
               :  |||||:|| ||:|||||||||||::   :: |  | | : :|  :|:|::| ||
Db        126 EITFYSSVLLLACISMDRYLAIVHATSTLIQKRHLV-KFVCITMWFLSLVLSLPIFILRT 184

Qy        177 VSEAD-DRYICDRFYPN-----DLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSK 230
                :|:    :|   | |       | || :      | :|| :::| ||   :  |  :
Db        185 TVKANPSTVVC---YENIGNNTSKWRVVLRILPQTYGFLLPLLIMLFCYGFTLRTLFKAH 241

Qy        231 GHQKRKALKTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEAL 290
               || :|::    ::| |  ||||| | :  |: :  ::||: || :| ::|    :| |
Db        242 MGQKHRAMRVIFAVVLVFLLCWLPYNIVLFTDTLMRTKLIKETCERQNEINK---ASEIL 298

Qy        291 AFFHCCLNPILYAFLGAKFKTSAQHALTSVSRGSSLKILSK---GKRGGHSSVSTESESS 347
               | | |||||:|||:| ||:    | |  :   ::  ::||    | |  | | : | ::
Db        299 GFLHSCLNPIIYAFIGQKFR----HGLLKIM--ANYGLVSKEFLAKEGRPSFVGSSSANT 352

Qy        348 S 348
              |
Db        353 S 353


RESULT 8
JC4587
chemokine (C-C) receptor 4 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: JC4587
R;Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
Biochem. Biophys. Res. Commun. 218, 337-343, 1996
A;Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to murine and human C
A;Reference number: JC4587; MUID:96136324; PMID:8573157
A;Accession: JC4587
```

```
A;Molecule type: mRNA
A;Residues: 1-360 <HOO>
A;Cross-references: UNIPROT:P51680; UNIPARC:UPI0000028F3B; EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:
A;Experimental source: thymus
C;Genetics:
A;Gene: cc ckr-4
C;Superfamily: vertebrate rhodopsin
C;Keywords: glycoprotein; phosphoprotein; receptor; thymus
F;2,183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

  Query Match             30.8%;  Score 564.5;  DB 2;  Length 360;
  Best Local Similarity   37.3%;  Pred. No. 1.7e-40;
  Matches  109;  Conservative   63;  Mismatches  117;  Indels    3;  Gaps    2;

Qy         21 YDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVMGYQKKLRSMTDKYRLHL 80
              |:|| :|| :|    | ::||| :||::|| |: || :|:||:   |:|:|||| | |:|
Db         22 YESMPKPCTKEGIKAFGEVFLPPLYSLVFLLGLFGNSVVVLVLFKYKRLKSMTDVYLLNL 81

Qy         81 SVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSSVLILAFISLDRYLAIVH 140
              :::||||||::||||   |   | ||  ||| |  :| |  || : .:  :|:||||||||
Db         82 AISDLLFVLSLPFWGYYAADQWVFGLGLCKIVSWMYLVGFYSGIFFIMLMSIDRYLAIVH 141

Qy        141 ATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEADDRYICDRFYP--NDLWVVV 198
              |  | : | |    :  :  |  |:  .::|  :|:      :   |   |   :  | |:
Db        142 AVFSLKARTLTYGVITSLITWSVAVFASLPGLLFSTCYTEHNHTYCKTQYSVNSTTWKVL 201

Qy        199 FQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTVILILAFFACWLPYYIG 258
                :  ::||::|  ::|  | :||  | | |  :| :|::    ::: |   |.|| :
Db        202 SSLEINVLGLLIPLGIMLFWYSMIIRTLQHCKNEKKNRAVRMIFGVVVLFLGFWTPYNVV 261

Qy        259 ISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPILYAFLGAKFK 310
              : ::: : ||:: | |  |  :   |  || | | ||||||::| ||| ||:
Db        262 LFLETLVELEVL-QDCTLERYLDYAIQATETLGFIHCCLNPVIYFFLGEKFR 312


RESULT 9
JQ1231
interleukin-8 receptor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: JQ1231; A46483
R;Beckmann, M.P.; Munger, W.E.; Kozlosky, C.; VandenBos, T.; Price, V.; Lyman, S.; Gerard, N.P.; Gerard, C.
Biochem. Biophys. Res. Commun. 179, 784-789, 1991
A;Title: Molecular characterization of the interleukin-8 receptor.
A;Reference number: JQ1231; MUID:91378994; PMID:1898400
A;Accession: JQ1231
A;Molecule type: DNA
A;Residues: 1-355 <BEC>
A;Cross-references: UNIPROT:P21109; UNIPARC:UPI000012D4ED; GB:M74240; NID:g165438; PIDN:AAA31375.1; PID:g16
R;Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
J. Immunol. 148, 1261-1264, 1992
A;Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor.
A;Reference number: A46483; MUID:92148149; PMID:1737938
A;Accession: A46483
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-355 <LEE>
A;Cross-references: UNIPARC:UPI000012D4ED; GB:M82873; NID:g165440; PIDN:AAA31376.1; PID:g165441
A;Experimental source: neutrophils
A;Note: sequence extracted from NCBI backbone (NCBIN:81526, NCBIP:81530)
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

  Query Match             30.8%;  Score 564;  DB 2;  Length 355;
  Best Local Similarity   35.0%;  Pred. No. 1.9e-40;
  Matches  123;  Conservative   71;  Mismatches  149;  Indels    8;  Gaps    6;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              |  :  :  | :    |    :    ||        ||  :  ||:::||  ::|| ||:
Db          8 MTDLWTWFEDEFANATGMPPVEKDYSPCL-VVTQTLNKYVVVVIYALVFLLSLLGNSLVM 66

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||: | :  ||:|| | |:|::|||||| :|:| |||     | ||  ||| | ::  ||
```

```
Db         67 LVILYSRSNRSVTDVYLLNLAMADLLFALTMPIWAVSKEKGWIFGTPLCKVVSLVKEVNF 126

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-SE 179
              || :|:|| ||:|||||||||| :   :: |  | : :|:|  :|:|::| |:|  | |
Db        127 YSGILLLACISVDRYLAIVHATRTLTQKRHLV-KFICLGIWALSLILSLPFFLFRQVFSP 185

Qy        180 ADDRYIC--DRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKA 237
               :   :|  |  :    | :| :      | ||| :|:| ||   :  |  :   || :|
Db        186 NNSSPVCYEDLGHNTAKWRMVLRILPHTFGFILPLLVMLFCYGFTLRTLFQAHMGQKHRA 245

Qy        238 LKTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCL 297
              ::    ::| |  ||||| : :  |: :   :|:: |:  | : : :  || | | | ||
Db        246 MRVIFAVVLIFLLCWLPYNLVLLADTLMRTHVIQETCQRRNDIDRALDATEILGFLHSCL 305

Qy        298 NPILYAFLGAKFKTSAQHALTSVSRG-SSLKILSKGKRGGHSSVSTESESS 347
              |||:|||:|  |:      |   :||  | : |:: :   ::| ||   |:
Db        306 NPIIYAFIGQNFRNGFLKML--AARGLISKEFLTRHRVTSYTSSSTNVPSN 354


RESULT 10
A55735
G protein-coupled receptor EBI1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A55735
R;Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
Genomics 23, 643-650, 1994.
A;Title: Cloning of human and mouse EBI1, a lymphoid-specific G-protein-coupled receptor encoded on human c
A;Reference number: A55735; MUID:95154835; PMID:7851893
A;Accession: A55735
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-378 <SCH>
A;Cross-references: UNIPROT:P47774; UNIPARC:UPI00000274D1; GB:L31580; NID:g468340; PIDN:AAA74232.1; PID:g46
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor

  Query Match             30.8%;  Score 563;  DB 2;  Length 378;
  Best Local Similarity   34.1%;  Pred. No. 2.4e-40;
  Matches  119;  Conservative   77;  Mismatches  147;  Indels    6;  Gaps    3;

Qy          9 SDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVMGYQKK 68
              :|:|  |  : ||   :  ||:::  ||   ||| :||:|   |::|||||||   | |:
Db         29 TDDYIGENTTVDYTLYESVCFKKDVRNFKAWFLPLMYSVICFVGLLGNGLVILTYIYFKR 88

Qy         69 LRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSSVLILA 128
              |::||| | |:|:|||:||:: |||||     :| || :||| :  || :: :| :|:|
Db         89 LKTMTDTYLLNLAVADILFLLILPFWAYSEAKSWIFGVYLCKGIFGIYKLSFFSGMLLLL 148

Qy        129 FISLDRYLAIVHAT--NSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV--SEADDRY 184
               ||:|||:||| |   :  | | ||  |:  ||:|: || |:||: ::: :  :  :|
Db        149 CISIDRYVAIVQAVSRHRHRARVLLISKLSCVGIWMLALFLSIPELLYSGLQKNSGEDTL 208

Qy        185 ICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTVIL 244
              |         ::  |   :: | ::| : :  || |||  |  ::  :: ||:|  : :
Db        209 RCSLVSAQVEALITIQVAQMVFGFLVPMLAMSFCYLIIIRTLLQARNFERNKAIKVIIAV 268

Qy        245 ILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPILYAF 304
              :: |    |||   :   :      |    ||    ::    :| :||   ||:|| ||||
Db        269 VVVFIVFQLPYNGVVLAQTVANFNITNSSCETSKQLNIAYDVTYSLASVRCCVNPFLYAF 328

Qy        305 LGAKFKTSAQHALTSVSRGSS--LKILSKGKRGGHSSVSTESESSSFHS 351
              :| ||::        :   |   |:  |  :   ::||| |:|:::  |
Db        329 IGVKFRSDLFKLFKDLGCLSQERLRHWSSCRHVRNASVSMEAETTTTFS 377


RESULT 11
A39445
interleukin-8 receptor type A - human
N;Alternate names: interleukin-8 receptor, high-affinity
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: I37449; I38710; I38711; A39445
R;Mollereau, C.; Muscatelli, F.; Mattei, M.G.; Vassart, G.; Parmentier, M.
Genomics 16, 248-251, 1993
A;Title: The high-affinity interleukin 8 receptor gene (IL8RA) maps to the 2q33-q36 region of the human gen
```

A;Reference number: I37449; MUID:93252387; PMID:8486366
A;Accession: I37449
A;Molecule type: DNA
A;Residues: 1-350 <RES>
A;Cross-references: UNIPROT:P25024; UNIPARC:UPI0000050457; EMBL:X65858; NID:g312046; PIDN:CAA46688.1; PID:g
R;Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
J. Biol. Chem. 269, 26381-26389, 1994
A;Title: Comparison of the genomic organization and promoter function for human interleukin-8 receptors A a
A;Reference number: I37898; MUID:95014476; PMID:7929358
A;Accession: I38710
A;Molecule type: DNA
A;Residues: 1-350 <RE2>
A;Cross-references: UNIPARC:UPI0000050457; EMBL:U11870; NID:g511804; PIDN:AAA64378.1; PID:g511805
A;Accession: I38711
A;Molecule type: mRNA
A;Residues: 1-16 <RE3>
A;Cross-references: UNIPARC:UPI000000053C; EMBL:U11871; NID:g511806; PIDN:AAA64379.1; PID:g733002
R;Holmes, W.E.; Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
Science 253, 1278-1280, 1991
A;Title: Structure and functional expression of a human interleukin-8 receptor.
A;Reference number: A39445; MUID:91368199; PMID:1840701
A;Accession: A39445
A;Molecule type: mRNA
A;Residues: 1-275,'T',277-350 <HOL>
A;Cross-references: UNIPARC:UPI0000043589; GB:M68932; NID:g186369; PIDN:AAA59159.1; PID:g186370
C;Genetics:
A;Gene: GDB:IL8RA
A;Cross-references: GDB:135039; OMIM:146929
A;Map position: 2q35-2q35
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; membrane protein

  Query Match 30.6%; Score 559.5; DB 2; Length 350;
  Best Local Similarity 38.2%; Pred. No. 4.5e-40;
  Matches 121; Conservative 56; Mismatches 127; Indels 13; Gaps 6;

```
Qy         11 NYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVMGYQKKLR 70
              |:|   |    |    ||   |    ||  :   |:::||  ::|| ||:||: | :  |
Db         16 NFT---GMPPADEDYSPCML-ETETLNKYVVIIAYALVFLLSLLGNSLVMLVILYSRVGR 71

Qy         71 SMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSSVLILAFI 130
              |:|| | |:|::||||| :||| ||   |  | || |||| | ::  || || :|:|| |
Db         72 SVTDVYLLNLALADLLFALTLPIWAASKVNGWIFGTFLCKVVSLLKEVNFYSGILLLACI 131

Qy        131 SLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEADDRY-ICDRF 189
              |:||||||||||| :   :: |  | | :| |  :: |::| |:|      ::   :|
Db        132 SVDRYLAIVHATRTLTQKRHLV-KFVCLGCWGLSMNLSLPFFLFRQAYHPNNSSPVCYEV 190

Qy        190 YPNDL--WVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTVILILA 247
                ||   | :| :      | |:|  |:| ||   :  |  :   || :|::    ::|
Db        191 LGNDTAKWRMVLRILPHTFGFIVPLFVMLFCYGFTLRTLFKAHMGQKHRAMRVIFAVVLI 250

Qy        248 FFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPILYAFLGA 307
              |  ||||| : :  |: :  ::|:: ||  | : : :  || | | | |||||:|||:|
Db        251 FLLCWLPYNLVLLADTLMRTQVIQESCERRNNIGRALDATEILGFLHSCLNPIIYAFIGQ 310

Qy        308 KF-----KTSAQHALTS 319
               |     |  | | | |
Db        311 NFRHGFLKILAMHGLVS 327
```

RESULT 12
A53752
interleukin-8 receptor (clone 5B1a) - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: A53752
R;Prado, G.N.; Thomas, K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Folco, E.; Navarro, J.
J. Biol. Chem. 269, 12391-12394, 1994
A;Title: Molecular characterization of a novel rabbit interleukin-8 receptor isotype.
A;Reference number: A53752; MUID:94230294; PMID:8175642
A;Accession: A53752
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-358 <PRA>
A;Cross-references: UNIPROT:P35344; UNIPARC:UPI000012D4F4; GB:L24445; NID:g437661; PIDN:AAA31378.1; PID:g43

C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 30.5%; Score 558; DB 2; Length 358;
Best Local Similarity 35.4%; Pred. No. 6.1e-40;
Matches 128; Conservative 66; Mismatches 138; Indels 30; Gaps 8;

```
Qy          7 YTSDNYTEEMGSGDYDSM----------KEPCFREENANFNKIFLPTIYSIIFLTGIV 54
              :| :||: |   ||: :              || | |:   |   :   | ::||  ::
Db          4 FTWENYSYEDFFGDFSNYSYSTDLPPTLLDSAPC-RSESLETNSYVVLITYILVFLLSLL 62

Qy         55 GNGLVILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHV 114
              || ||:||: | :   |:|| | |:|::|||||  ||| ||   |  | ||  ||| | :
Db         63 GNSLVMLVILYSRSTCSVTDVYLLNLAIADLLFATTLPIWAASKVHGWTFGTPLCKVVSL 122

Qy        115 IYTVNLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIF 174
              :  || || :|:|| ||:||||||||||| :   :: |  | : : :|  :|:|::|  :|
Db        123 VKEVNFYSGILLLACISVDRYLAIVHATRTMIQKRHLV-KFICLSMWGVSLILSLPILLF 181

Qy        175 AN-VSEADDRYICDRFYPNDL--WVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKG 231
               | :   :   :|     |    | :| :      | ||| :|:| ||   :  |  :
Db        182 RNAIFPPNSSPVCYEDMGNSTAKWRMVLRILPQTFGFILPLLVMLFCYVFTLRTLFQAHM 241

Qy        232 HQKRKALKTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALA 291
               || :|::    ::| |  ||||| : :  |: :   :|:: ||  | : : :  || |
Db        242 GQKHRAMRVIFAVVLIFLLCWLPYNLVLLTDTLMRTHVIQETCERRNDIDRALDATEILG 301

Qy        292 FFHCCLNPILYAFLGAKF-----KTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESES 346
              | | |||||:|||:| ||     |  | | |       | : |:|  |   | |:: | :
Db        302 FLHSCLNPIIYAFIGQKFRYGLLKILAAHGLI------SKEFLAKESR--PSFVASSSGN 353

Qy        347 SS 348
              :|
Db        354 TS 355
```

RESULT 13
B55735
lymphocyte-specific G protein-coupled receptor EBI1 - human
N;Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: B55735; S52443
R;Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
Genomics 23, 643-650, 1994
A;Title: Cloning of human and mouse EBI1, a lymphoid-specific G-protein-coupled receptor encoded on human c
A;Reference number: A55735; MUID:95154835; PMID:7851893
A;Accession: B55735
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-378 <SCH>
A;Cross-references: UNIPROT:P32248; UNIPARC:UPI0000001C2F; GB:L31581; NID:g468319; PIDN:AAA74231.1; PID:g46
R;Burgstahler, R.; Kempkes, B.; Staeube, K.; Lipp, M.
submitted to the EMBL Data Library, February 1995
A;Description: The expression of the chemokine receptor BLR2/EBI1 is specifically transactivated by Epstein
A;Reference number: S52443
A;Accession: S52443
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 21-378 <BUR>
A;Cross-references: UNIPARC:UPI000014DEAD; EMBL:X84702
C;Genetics:
A;Gene: GDB:CMKBR7; EBI1; BLR2; CCR7
A;Cross-references: GDB:342065; OMIM:600242
A;Map position: 17q12-17q21.2
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor

Query Match 30.4%; Score 557; DB 2; Length 378;
Best Local Similarity 33.2%; Pred. No. 7.9e-40;
Matches 116; Conservative 79; Mismatches 148; Indels 6; Gaps 3;

```
Qy          9 SDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVMGYQKK 68
              :|:|  :  : ||   :  | :::  ||   ||| :|||   |::|||||:|   | |:
Db         29 TDDYIGDNTTVDYTLFESLCSKKDVRNFKAWFLPIMYSIICFVGLLGNGLVVLTYIYFKR 88
```

```
Qy         69 LRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSSVLILA 128
              |::||| | |:|:|||:||::|||||| | :| ||  || : || :: :| :|:|
Db         89 LKTMTDTYLLNLAVADILFLLTLPFWAYSAAKSWVFGVHFCKLIFAIYKMSFFSGMLLLL 148

Qy        129 FISLDRYLAIVHATNS--QRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV--SEADDRY 184
              ||:|||:||| | ::   | | ||  |:  ||:|| | :|:||: ::::: | ::
Db        149 CISIDRYVAIVQAVSAHRHRARVLLISKLSCVGIWILATVLSIPELLYSDLQRSSSEQAM 208

Qy        185 ICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTVIL 244
              |     :    : |   :::| ::| : :  || :|| |  ::  :: ||:|  : :
Db        209 RCSLITEHVEAFITIQVAQMVIGFLVPLLAMSFCYLVIIRTLLQARNFERNKAIKVIIAV 268

Qy        245 ILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPILYAF 304
              :: |    |||   :   :     |    ||    ::    :| :||   ||:|| ||||
Db        269 VVVFIVFQLPYNGVVLAQTVANFNITSSTCELSKQLNIAYDVTYSLACVRCCVNPFLYAF 328

Qy        305 LGAKFKTSAQHALTSVS--RGSSLKILSKGKRGGHSSVSTESESSSFHS 351
              :| ||:         :       |:  |  :    ||:| |:|::  |
Db        329 IGVKFRNDLFKLFKDLGCLSQEQLRQWSSCRHIRRSSMSVEAETTTTFS 377


RESULT 14
JC4304
orphan G protein-coupled receptor - human
N;Alternate names: V28 protein
C;Species: Homo sapiens (man)
C;Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: JC4304
R;Raport, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
Gene 163, 295-299, 1995
A;Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related to genes for chemokine
A;Reference number: JC4304; MUID:96011651; PMID:7590284
A;Accession: JC4304
A;Molecule type: mRNA
A;Residues: 1-355 <RAP>
A;Cross-references: UNIPROT:P49238; UNIPARC:UPI0000000AOB; GB:U20350; NID:g665580; PIDN:AAA91783.1; PID:g66
A;Experimental source: peripheral blood mononuclear cell
C;Comment: This protein is a cell-surface receptor which recognizes extracellular signals and transduces th
C;Comment: This protein is a key regulator of many immune and homeostatic responses, and interacts between
C;Genetics:
A;Gene: v28
A;Map position: 3pter-p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; lymphokine; transmembrane protein
F;35-57/Domain: transmembrane #status predicted <TM1>
F;66-88/Domain: transmembrane #status predicted <TM2>
F;104-125/Domain: transmembrane #status predicted <TM3>
F;146-165/Domain: transmembrane #status predicted <TM4>
F;197-217/Domain: transmembrane #status predicted <TM5>
F;230-254/Domain: transmembrane #status predicted <TM6>
F;275-296/Domain: transmembrane #status predicted <TM7>

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  Best Local Similarity  33.2%;  Pred. No. 3.2e-39;
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Qy         10 DNYTEEMGSG-DYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVMGYQKK 68
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Db          2 DQFPESVTENFEYDDLAEACYIGDIVVFGTVFLSIFYSVIFAIGLVGNLLVVFALTNSKK 61

Qy         69 LRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSSVLILA 128
              :|:|| | |:|:::|||||| |||||    :      | :||     : :  : |:  :
Db         62 PKSVTDIYLLNLALSDLLFVATLPFWTHYLINEKGLHNAMCKFTTAFFFIGFFGSIFFIT 121

Qy        129 FISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEADDRYICDR 188
              ||:|||||||| | ||   | :     : :|||  |:|:  | |:|    | :    |
Db        122 VISIDRYLAIVLAANSMNNRTVQHGVTISLGVWAAAILVAAPQFMFTKQKENE----CLG 177

Qy        189 FYP---NDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTVILI 245
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Db        178 DYPEVLQEIWPVLRNVETNFLGFLLPLLIMSYCYFRIIQTLFSCKNHKKAKAIKLILLVV 237

Qy        246 LAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPILYAFL 305
              : ||  | || : | :::  | :     |:   :   :|:|| :|| |||||::|||
Db        238 IVFFLFWTPYNVMIFLETLKLYDFF-PSCDMRKDLRLALSVTETVAFSHCCLNPLIYAFA 296
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Qy        306 GAKFKTSAQHALTSVSRGSSLKIL----------SKGKRGGHSSVSTESESSSFHSS 352
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Db        297 GEKFRRYLYHLY-----GKCLAVLCGRSVHVDFSSSESQRSRHGSVL--SSNFTYHTS 347


RESULT 15
S56162
MDCR15 protein - human
C;Species: Homo sapiens (man)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999
C;Accession: S56162
R;Barella, L.; Loetscher, M.; Tobler, A.; Baggiolini, M.; Moser, B.
Biochem. J. 309, 773-779, 1995
A;Title: Sequence variation of a novel heptahelical leucocyte receptor through alternative transcript forma
A;Reference number: S56162; MUID:95366951; PMID:7639692
A;Accession: S56162
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-327 <BAR>
A;Cross-references: UNIPARC:UPI000016AD1F; EMBL:X68829; NID:g840783; PIDN:CAA48723.1; PID:g840784
C;Superfamily: vertebrate rhodopsin

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  Best Local Similarity   34.2%;  Pred. No. 8.7e-39;
  Matches  113;  Conservative   70;  Mismatches  123;  Indels   24;  Gaps    4;

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              |:|  :|:|  ||:||| |::|| ||:::::   :: || |: :  ||:|||| |  |||
Db          2 ASFKAVFVPVAYSLIFLLGVIGNVLVLVILERHRQTRSSTETFLFHLAVADLLLVFILPF 61

Qy         94 WAVDAVANWYFGNFLCKAVHVIYTVNLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAE 153
                 :    |  | |||| |  :: || | | |:|| |::|||||||||| :: | |:||:
Db         62 AVAEGSVGWVLGTFLCKTVIALHKVNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSI 121

Qy        154 KVVYVGVWIPALLLTIPDFIFANVSEADDRYICDRFYPNDLWVVVF-------------- 199
               :    :|:   || :|: :|| ||:          : | |    |
Db        122 HITCGTIWLVGFLLALPEILFAKVSQG--------HHNNSLPRCTFSQENQAETHAWFTS 173

Qy        200 QFQHIMVGLILPGIVILSCYCIIISKLSHSKGH-QKRKALKTTVILILAFFACWLPYYIG 258
              :| : : | :|| :|:  ||  :: :|  ::   |::||::  :::   || || ||:|
Db        174 RFLYHVAGFLLPMLVMGWCYVGVVHRLRQAQRRPQRQKAVRVAILVTSIFFLCWSPYHIV 233

Qy        259 ISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPILYAFLGAKFKTSAQHALT 318
              | :|:   |: :   |:   ::   |:: | |   ||||||:|| | | ||::     ||
Db        234 IFLDTLARLKAVDNTCKLNGSLPVAITMCEFLGLAHCCLNPMLYTFAGVKFRSDLSRLLT 293

Qy        319 SVSRGSSLKILSKGKRGGHSSVSTESESSS 348
               :   |   :          ||:| |||:::
Db        294 KLGCTSPASLCQLFPSWRRSSLS-ESENAT 322


Search completed: February 6, 2007, 14:23:54
Job time : 26.744 secs
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start

SCORE Search Results Details for Application 10785230 and Search Result 20070206_074033_us-10-785-230-1.rapbm.

This page gives you Search Results detail for the Application 10785230 and Search Result 20070206_074033_us-10-785-230-1.rapbm.

start

Go Back to previous page

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                          GenCore version 6.2
                    Copyright (c) 1993 - 2007  Biocceleration Ltd.


OM protein - protein search, using sw model

Run on:         February  6, 2007, 14:24:16 ; Search time 134 Seconds
                                        (without alignments)
                                        1215.298 Million cell updates/sec

Title:          US-10-785-230-1
Perfect score:  1830
Sequence:       1 MEGISIYTSDNYTEEMGSGD.........KRGGHSSVSTESESSSFHSS 352

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters:    2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        Published_Applications_AA_Main:*
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                3:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
                4:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
                5:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                    SUMMARIES

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Result           Query
   No.    Score  Match  Length DB  ID                          Description
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     1     1830  100.0     352  3  US-09-953-692-2             Sequence 2, Appli
     2     1830  100.0     352  3  US-09-953-717-2             Sequence 2, Appli
     3     1830  100.0     352  3  US-09-104-063-4             Sequence 4, Appli
     4     1830  100.0     352  3  US-09-813-651B-85           Sequence 85, Appl
     5     1830  100.0     352  4  US-10-151-274-4             Sequence 4, Appli
     6     1830  100.0     352  4  US-10-225-567A-76           Sequence 76, Appl
     7     1830  100.0     352  4  US-10-245-850-1             Sequence 1, Appli
     8     1830  100.0     352  4  US-10-251-703-38            Sequence 38, Appl
     9     1830  100.0     352  4  US-10-021-660-123           Sequence 123, App
    10     1830  100.0     352  4  US-10-014-322A-126          Sequence 126, App
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11	1830	100.0	352	4	US-10-239-423-79	Sequence 79, Appl
12	1830	100.0	352	4	US-10-170-385-331	Sequence 331, App
13	1830	100.0	352	4	US-10-160-401-3	Sequence 3, Appli
14	1830	100.0	352	4	US-10-341-434-178	Sequence 178, App
15	1830	100.0	352	4	US-10-372-683-2	Sequence 2, Appli
16	1830	100.0	352	4	US-10-440-464-78	Sequence 78, Appl
17	1830	100.0	352	4	US-10-452-015-1	Sequence 1, Appli
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20	1830	100.0	352	4	US-10-181-906-10	Sequence 10, Appl
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22	1830	100.0	352	4	US-10-785-230-1	Sequence 1, Appli
23	1830	100.0	352	5	US-10-486-471-20	Sequence 20, Appl
24	1830	100.0	352	5	US-10-985-324-2	Sequence 2, Appli
25	1830	100.0	352	6	US-11-021-951-189	Sequence 189, App
26	1830	100.0	352	6	US-11-028-922A-1	Sequence 1, Appli
27	1824	99.7	352	3	US-09-826-509-485	Sequence 485, App
28	1824	99.7	352	5	US-10-925-095-485	Sequence 485, App
29	1822	99.6	352	3	US-09-870-759-37	Sequence 37, Appl
30	1822	99.6	352	3	US-09-870-759-144	Sequence 144, App
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32	1822	99.6	352	3	US-09-751-708A-144	Sequence 144, App
33	1822	99.6	352	4	US-10-428-817A-33	Sequence 33, Appl
34	1822	99.6	352	4	US-10-428-817A-140	Sequence 140, App
35	1822	99.6	352	5	US-10-937-758A-37	Sequence 37, Appl
36	1822	99.6	352	5	US-10-937-758A-121	Sequence 121, App
37	1808	98.8	356	5	US-10-723-860-1280	Sequence 1280, Ap
38	1789	97.8	352	5	US-10-791-592-6	Sequence 6, Appli
39	1789	97.8	352	5	US-10-791-166-6	Sequence 6, Appli
40	1785	97.5	348	5	US-10-330-773-921	Sequence 921, App
41	1678.5	91.7	359	4	US-10-785-230-3	Sequence 3, Appli
42	1673	91.4	349	6	US-11-028-922A-2	Sequence 2, Appli
43	1633.5	89.3	355	5	US-10-330-773-918	Sequence 918, App
44	1042	56.9	209	4	US-10-292-798-688	Sequence 688, App
45	1037	56.7	209	4	US-10-017-161-790	Sequence 790, App

ALIGNMENTS

RESULT 1
US-09-953-692-2
; Sequence 2, Application US/09953692
; Patent No. US20020107195A1
; GENERAL INFORMATION:
; APPLICANT: Shalley, Gupta K.
; TITLE OF INVENTION: Method for Inducing Chemotaxis in Endothelial Cells by
; TITLE OF INVENTION: Administering Stromal Cell Derived Factor-1(
; FILE REFERENCE: P50676C1
; CURRENT APPLICATION NUMBER: US/09/953,692
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 09/358,624
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 60/093,596
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Human
US-09-953-692-2

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Best Local Similarity 100.0%; Pred. No. 1.6e-157;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
                ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 2
US-09-953-717-2
; Sequence 2, Application US/09953717
; Patent No. US20020107196A1
; GENERAL INFORMATION:
;  APPLICANT: Shalley, Gupta K.
;  TITLE OF INVENTION: Method for Inducing Chemotaxis in Endothelial Cells by
;  TITLE OF INVENTION:  Administering Stromal Cell Derived Factor-1(
;  FILE REFERENCE: P50676D1
;  CURRENT APPLICATION NUMBER: US/09/953,717
;  CURRENT FILING DATE:  2001-09-17
;  PRIOR APPLICATION NUMBER: 09/358,624
;  PRIOR FILING DATE: 1999-07-21
;  PRIOR APPLICATION NUMBER: 60/093,596
;  PRIOR FILING DATE: 1998-07-21
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Human
US-09-953-717-2

  Query Match             100.0%;  Score 1830;  DB 3;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-157;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
                ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 3
US-09-104-063-4
; Sequence 4, Application US/09104063
; Patent No. US20020168356A1
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, James
;    APPLICANT:  Wood, William I.
;    TITLE OF INVENTION:  PF4A Receptors
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;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/104,063
;      FILING DATE:  24-June-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/701265
;      FILING DATE:  22-AUG-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/664228
;      FILING DATE:  06-JUN-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/076093
;      FILING DATE:  11-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/810782
;      FILING DATE:  19-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P0706P2C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  352 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-09-104-063-4

  Query Match             100.0%;  Score 1830;  DB 3;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-157;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
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Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
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Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
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Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 4
US-09-813-651B-85
; Sequence 85, Application US/09813651B
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; Publication No. US20030018438A1
; GENERAL INFORMATION:
; APPLICANT: Nestor, John
; APPLICANT: Wilson, Carol
; APPLICANT: Tan Hehir, Christina
; APPLICANT: Kates, Steven
; TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compounds
; FILE REFERENCE: CNS-007
; CURRENT APPLICATION NUMBER: US/09/813,651B
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 85
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-651B-85

Query Match 100.0%; Score 1830; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.6e-157;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
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RESULT 5
US-10-151-274-4
; Sequence 4, Application US/10151274
; Publication No. US20030064071A1
; GENERAL INFORMATION:
; APPLICANT: Littman, Dan R.
; APPLICANT: Kwon, Douglas S.
; APPLICANT: van Kooyk, Yvette
; APPLICANT: Geijtenbeck, Tneo
; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY
; TITLE OF INVENTION: INTO
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 1049-1-017
; CURRENT APPLICATION NUMBER: US/10/151,274
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US/09/517,605
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-151-274-4

Query Match 100.0%; Score 1830; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.6e-157;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
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RESULT 6
US-10-225-567A-76
; Sequence 76, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS (GPCRS)
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-76

Query Match 100.0%; Score 1830; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.6e-157;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 7
US-10-245-850-1
; Sequence 1, Application US/10245850
; Publication No. US20030124628A1
; GENERAL INFORMATION:
;  APPLICANT: Burns, Jennifer M.
;  APPLICANT:  Miao, Zhenhua
;  APPLICANT:  Wei, Zheng
;  APPLICANT:  Howard, Maureen C.
;  APPLICANT:  Premack, Brett A.
;  APPLICANT:  Schall, Thomas J.
;  APPLICANT:  ChemoCentryx, Inc.
;  TITLE OF INVENTION: Compositions and Methods for Detecting and Treating
;  TITLE OF INVENTION:  Diseases and Conditions Related to Chemokine Receptors
;  FILE REFERENCE: 019934-003310US
;  CURRENT APPLICATION NUMBER: US/10/245,850
;  CURRENT FILING DATE:  2002-09-16
;  PRIOR APPLICATION NUMBER: US 60/338,100
;  PRIOR FILING DATE: 2001-11-30
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: CXCR4 chemokine receptor
US-10-245-850-1

  Query Match             100.0%;  Score 1830;  DB 4;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-157;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 8
US-10-251-703-38
; Sequence 38, Application US/10251703
; Publication No. US20030148449A1
; GENERAL INFORMATION:
;  APPLICANT: Kuliopulos, Athan
;  APPLICANT:  Covic, Lidija
;  TITLE OF INVENTION: G Protein Coupled Receptor Agonists and Antagonists and
;  TITLE OF INVENTION:  Methods of Activating and Inhibiting G Protein Coupled
;  TITLE OF INVENTION:  Receptors Using the Same
;  FILE REFERENCE: NEMC-215 CIP
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;  CURRENT APPLICATION NUMBER: US/10/251,703
;  CURRENT FILING DATE:  2002-09-20
;  PRIOR APPLICATION NUMBER: 09/841,091
;  PRIOR FILING DATE: 2001-04-23
;  PRIOR APPLICATION NUMBER: 60/198,993
;  PRIOR FILING DATE: 2000-04-21
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Pepducin
;   OTHER INFORMATION: Peptide Sequence
US-10-251-703-38

  Query Match             100.0%;  Score 1830;  DB 4;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-157;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 9
US-10-021-660-123
; Sequence 123, Application US/10021660
; Publication No. US20030152926A1
; GENERAL INFORMATION:
;  APPLICANT: Murray, Richard
;  APPLICANT:  Glynne, Richard
;  APPLICANT:  Watson, Susan R.
;  APPLICANT:  EOS Biotechnology, Inc.
;  TITLE OF INVENTION: No. US20030152926A1el Methods of Diagnosis of Angiogenesis,
;  TITLE OF INVENTION:  Compositions and Methods of Screening for Angiogenesis
;  TITLE OF INVENTION:  Modulators
;  FILE REFERENCE: 018501-000710US
;  CURRENT APPLICATION NUMBER: US/10/021,660
;  CURRENT FILING DATE:  2001-12-06
;  PRIOR APPLICATION NUMBER: US/09/784,356
;  PRIOR FILING DATE: 2001-02-14
;  PRIOR APPLICATION NUMBER: US 09/637,977
;  PRIOR FILING DATE: 2000-08-11
;  NUMBER OF SEQ ID NOS: 135
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 123
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-021-660-123

  Query Match             100.0%;  Score 1830;  DB 4;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-157;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 10
US-10-014-322A-126
; Sequence 126, Application US/10014322A
; Publication No. US20030167129A1
; GENERAL INFORMATION:
;  APPLICANT: Nestor, Jr., John
;  APPLICANT:  Wilson, Carol
;  APPLICANT:  Tan Hehir, Christina
;  APPLICANT:  Kates, Steven
;  APPLICANT:  Krstenansky, John
;  TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compounds
;  FILE REFERENCE: CNS-008
;  CURRENT APPLICATION NUMBER: US/10/014,322A
;  CURRENT FILING DATE:  2002-07-08
;  PRIOR APPLICATION NUMBER: US 60/243,587
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: US 09/813,651
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: US 09/813,653
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: US 09/813,448
;  PRIOR FILING DATE: 2001-03-20
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 126
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-014-322A-126

  Query Match            100.0%;  Score 1830;  DB 4;  Length 352;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-157;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
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Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 11
US-10-239-423-79
; Sequence 79, Application US/10239423
; Publication No. US20030186889A1
; GENERAL INFORMATION:
;  APPLICANT: FORSSMANN, Wolf-Georg; FORSSMANN, Ulf; ADERMANN, Knut;
;  APPLICANT:  HEITLAND, Aleksandra; SPODSBERG, Nikolaj
;  TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
;  TITLE OF INVENTION:  Cell Surface Proteome of Tumor and Inflammation Cells and
;  TITLE OF INVENTION:  for Treating Tumor Diseases and Inflammatory Diseases,
;  TITLE OF INVENTION:  Preferably with the Aid of Specific Chemokine
;  TITLE OF INVENTION:  Receptor Analysis and Chemokine Receptor/Ligand Interaction
;  FILE REFERENCE: 022217us
;  CURRENT APPLICATION NUMBER: US/10/239,423
;  CURRENT FILING DATE:  2002-09-23
;  PRIOR APPLICATION NUMBER: DE10016013.1
;  PRIOR FILING DATE: 2000-03-31
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
US-10-239-423-79

  Query Match             100.0%;  Score 1830;  DB 4;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-157;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
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Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
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Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
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Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
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Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 12
US-10-170-385-331
; Sequence 331, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
;  APPLICANT: Ward, Neil Raymond
;  APPLICANT:  Mundy, Christopher Robert
;  APPLICANT:  Kan, On
;  APPLICANT:  Harris, Robert Alan
;  APPLICANT:  White, Jonathan
```

```
;  APPLICANT:  Binley, Katie Mary
;  APPLICANT:  Rayner, William Nigel
;  APPLICANT:  Naylor, Stuart
;  APPLICANT:  Kingsman, Susan Mary
;  APPLICANT:  Krige, David
;  TITLE OF INVENTION: ANALYSIS METHOD
;  FILE REFERENCE: 532682000100
;  CURRENT APPLICATION NUMBER: US/10/170,385
;  CURRENT FILING DATE:  2002-06-12
;  PRIOR APPLICATION NUMBER: PCT/GB02/01662
;  PRIOR FILING DATE: 2002-04-08
;  PRIOR APPLICATION NUMBER: PCT/GB01/05458
;  PRIOR FILING DATE: 2001-12-10
;  NUMBER OF SEQ ID NOS: 549
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 331
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-170-385-331

  Query Match             100.0%;  Score 1830;  DB 4;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-157;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
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Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
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Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
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Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 13
US-10-160-401-3
; Sequence 3, Application US/10160401
; Publication No. US20030207281A1
; GENERAL INFORMATION:
;  APPLICANT: Genaissance Pharmaceuticals, Inc.
;  APPLICANT:  Bentivegna, Steven C.
;  APPLICANT:  Bieglecki, Karyn M.
;  APPLICANT:  Koshy, Beena
;  APPLICANT:  Monroe, Glen
;  APPLICANT:  Rounds, Eileen
;  TITLE OF INVENTION: HAPLOTYPES OF THE CXCR4 GENE
;  FILE REFERENCE: MWH-0121US
;  CURRENT APPLICATION NUMBER: US/10/160,401
;  CURRENT FILING DATE:  2002-05-03
;  PRIOR APPLICATION NUMBER: PCT/US01/12268
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: US 60/197,025
;  PRIOR FILING DATE: 2000-04-13
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-160-401-3
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  Query Match             100.0%;  Score 1830;  DB 4;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-157;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
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Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
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RESULT 14
US-10-341-434-178
; Sequence 178, Application US/10341434
; Publication No. US20030215835A1
; GENERAL INFORMATION:
;  APPLICANT: OriGene Technologies
;  TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
;  FILE REFERENCE: 9U 204 205 R1
;  CURRENT APPLICATION NUMBER: US/10/341,434
;  CURRENT FILING DATE:  2003-07-18
;  PRIOR APPLICATION NUMBER: US 60/348,164
;  PRIOR FILING DATE: 2002-01-15
;  PRIOR APPLICATION NUMBER: US 60/348,119
;  PRIOR FILING DATE: 2002-01-15
;  NUMBER OF SEQ ID NOS: 238
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 178
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-341-434-178

  Query Match             100.0%;  Score 1830;  DB 4;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-157;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
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Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
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Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
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Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
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Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 15
US-10-372-683-2
; Sequence 2, Application US/10372683
; Publication No. US20040009171A1
; GENERAL INFORMATION:
;  APPLICANT: GERRITSEN, MARY E.
;  APPLICANT:  PEALE JR., FRANKLIN V.
;  APPLICANT:  WU, THOMAS D.
;  TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA
;  FILE REFERENCE: P1928R1P1
;  CURRENT APPLICATION NUMBER: US/10/372,683
;  CURRENT FILING DATE:  2003-02-21
;  PRIOR APPLICATION NUMBER: US 10/271,690
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: US 60/344,534
;  PRIOR FILING DATE: 2001-10-18
;  NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 2
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-10-372-683-2

  Query Match             100.0%;  Score 1830;  DB 4;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-157;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
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Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
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Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
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Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
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Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


Search completed: February  6, 2007, 14:29:54
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SCORE 1.3 BuildDate: 11/17/2006

SCORE Search Results Details for Application 10785230 and Search Result 20070206_074037_us-10-785-230-1.rapbn.

This page gives you Search Results detail for the Application 10785230 and Search Result 20070206_074037_us-10-785-230-1.rapbn.

start

Go Back to previous page

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                          GenCore version 6.2
                    Copyright (c) 1993 - 2007  Biocceleration Ltd.


OM protein - protein search, using sw model

Run on:          February  6, 2007, 14:25:40 ; Search time 41 Seconds
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Title:           US-10-785-230-1
Perfect score:   1830
Sequence:        1 MEGISIYTSDNYTEEMGSGD.........KRGGHSSVSTESESSSFHSS 352

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Searched:        571941 seqs, 137706945 residues

Total number of hits satisfying chosen parameters:      571941

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                    SUMMARIES

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  No.    Score      Match  Length  DB  ID                          Description
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    1     1830      100.0     352   6  US-10-505-928-745           Sequence 745, App
    2     1830      100.0     352   6  US-10-511-937-2486          Sequence 2486, Ap
    3     1830      100.0     352   6  US-10-511-937-2935          Sequence 2935, Ap
    4     1830      100.0     352   6  US-10-511-937-3010          Sequence 3010, Ap
    5     1830      100.0     352   6  US-10-219-051B-9078         Sequence 9078, Ap
    6     1830      100.0     352   6  US-10-219-051B-9082         Sequence 9082, Ap
    7     1830      100.0     352   7  US-11-371-354-68409         Sequence 68409, A
    8     1827       99.8     363   6  US-10-545-557-19            Sequence 19, Appl
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9	1824	99.7	352	7	US-11-404-939-485	Sequence 485, App
10	1785	97.5	348	6	US-10-540-898-921	Sequence 921, App
11	1678.5	91.7	359	7	US-11-437-734-2	Sequence 2, Appli
12	1673	91.4	349	6	US-10-219-051B-9076	Sequence 9076, Ap
13	1673	91.4	349	6	US-10-219-051B-9080	Sequence 9080, Ap
14	1671.5	91.3	352	7	US-11-437-734-8	Sequence 8, Appli
15	1633.5	89.3	355	6	US-10-540-898-918	Sequence 918, App
16	1100.5	60.1	230	7	US-11-437-734-4	Sequence 4, Appli
17	1042	56.9	209	7	US-11-214-063A-688	Sequence 688, App
18	850	46.4	188	7	US-11-437-734-6	Sequence 6, Appli
19	600.5	32.8	360	6	US-10-581-413-1	Sequence 1, Appli
20	581.5	31.8	359	6	US-10-219-051B-13793	Sequence 13793, A
21	576.5	31.5	368	6	US-10-511-937-2505	Sequence 2505, Ap
22	576.5	31.5	368	6	US-10-511-937-2931	Sequence 2931, Ap
23	576.5	31.5	368	7	US-11-302-678-59	Sequence 59, Appl
24	576.5	31.5	368	7	US-11-371-354-63307	Sequence 63307, A
25	569	31.1	367	7	US-11-392-789-2	Sequence 2, Appli
26	568	31.0	360	6	US-10-533-519-1184	Sequence 1184, Ap
27	568	31.0	360	6	US-10-219-051B-13795	Sequence 13795, A
28	568	31.0	360	7	US-11-242-111-19	Sequence 19, Appl
29	568	31.0	360	7	US-11-371-354-67277	Sequence 67277, A
30	563.5	30.8	350	7	US-11-371-354-61621	Sequence 61621, A
31	560.5	30.6	369	7	US-11-371-354-69405	Sequence 69405, A
32	560	30.6	374	6	US-10-669-920-3	Sequence 3, Appli
33	559.5	30.6	350	7	US-11-371-354-68399	Sequence 68399, A
34	559	30.5	361	6	US-10-669-920-374	Sequence 374, App
35	557.5	30.5	357	7	US-11-371-354-66939	Sequence 66939, A
36	557	30.4	378	6	US-10-511-937-2404	Sequence 2404, Ap
37	557	30.4	389	6	US-10-545-557-23	Sequence 23, Appl
38	557	30.4	475	7	US-11-520-715-56811	Sequence 56811, A
39	554.5	30.3	369	7	US-11-404-939-481	Sequence 481, App
40	553.5	30.2	364	6	US-10-669-920-377	Sequence 377, App
41	550	30.1	374	6	US-10-669-920-6	Sequence 6, Appli
42	549.5	30.0	355	6	US-10-516-032-8	Sequence 8, Appli
43	549.5	30.0	355	6	US-10-533-519-1109	Sequence 1109, Ap
44	549.5	30.0	355	7	US-11-371-354-56785	Sequence 56785, A
45	530	29.0	325	6	US-10-669-920-237	Sequence 237, App

ALIGNMENTS

RESULT 1
US-10-505-928-745
; Sequence 745, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 745
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-745

Query Match 100.0%; Score 1830; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.1e-164;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
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Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 2
US-10-511-937-2486
; Sequence 2486, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
;  APPLICANT: EXPRESSION DIAGNOSTICS, INC.
;  APPLICANT:  Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  APPLICANT:  Prentice, James
;  APPLICANT:  Morris, MacDonald
;  APPLICANT:  Rosenberg, Steven
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
;  TITLE OF INVENTION:  AND MONITORING TRANSPLANT REJECTION
;  FILE REFERENCE: 506612000104
;  CURRENT APPLICATION NUMBER: US/10/511,937
;  CURRENT FILING DATE:  2004-10-19
;  PRIOR APPLICATION NUMBER: PCT/US2003/012946
;  PRIOR FILING DATE: 2003-04-24
;  PRIOR APPLICATION NUMBER: US 10/131,831
;  PRIOR FILING DATE: 2002-04-24
;  PRIOR APPLICATION NUMBER: US 10/325,899
;  PRIOR FILING DATE: 2002-12-20
;  NUMBER OF SEQ ID NOS: 3117
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2486
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-511-937-2486

  Query Match            100.0%;  Score 1830;  DB 6;  Length 352;
  Best Local Similarity  100.0%;  Pred. No. 3.1e-164;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
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RESULT 3
US-10-511-937-2935
; Sequence 2935, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
;  APPLICANT: EXPRESSION DIAGNOSTICS, INC.
;  APPLICANT:  Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  APPLICANT:  Prentice, James
;  APPLICANT:  Morris, MacDonald
;  APPLICANT:  Rosenberg, Steven
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
;  TITLE OF INVENTION:  AND MONITORING TRANSPLANT REJECTION
;  FILE REFERENCE: 506612000104
;  CURRENT APPLICATION NUMBER: US/10/511,937
;  CURRENT FILING DATE:  2004-10-19
;  PRIOR APPLICATION NUMBER: PCT/US2003/012946
;  PRIOR FILING DATE: 2003-04-24
;  PRIOR APPLICATION NUMBER: US 10/131,831
;  PRIOR FILING DATE: 2002-04-24
;  PRIOR APPLICATION NUMBER: US 10/325,899
;  PRIOR FILING DATE: 2002-12-20
;  NUMBER OF SEQ ID NOS: 3117
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2935
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-511-937-2935

  Query Match           100.0%;  Score 1830;  DB 6;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-164;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 4
US-10-511-937-3010
; Sequence 3010, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
;  APPLICANT: EXPRESSION DIAGNOSTICS, INC.
;  APPLICANT:  Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  APPLICANT:  Prentice, James
;  APPLICANT:  Morris, MacDonald
;  APPLICANT:  Rosenberg, Steven
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
;  TITLE OF INVENTION:  AND MONITORING TRANSPLANT REJECTION
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; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3010
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-511-937-3010

  Query Match   100.0%; Score 1830; DB 6; Length 352;
  Best Local Similarity   100.0%; Pred. No. 3.1e-164;
  Matches 352; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy   61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy   121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy   181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy   241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy   301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352

RESULT 5
US-10-219-051B-9078
; Sequence 9078, Application US/10219051B
; Publication No. US20070015145A1
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: LeA 35693 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/219,051B
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/312,147
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/346,382
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/333,347
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 14715
; SOFTWARE: Perl script
; SEQ ID NO 9078
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: SWISS-Prot / P30991
;   DATABASE ENTRY DATE: 2002-06-15
US-10-219-051B-9078

  Query Match   100.0%; Score 1830; DB 6; Length 352;
  Best Local Similarity   100.0%; Pred. No. 3.1e-164;

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  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 6
US-10-219-051B-9082
; Sequence 9082, Application US/10219051B
; Publication No. US20070015145A1
; GENERAL INFORMATION:
;  APPLICANT: The General Hospital Corporation doing business as Massachusetts General
;  APPLICANT:  Hospital / Bayer AG
;  TITLE OF INVENTION: Nucleotide sequences involved in pain
;  FILE REFERENCE: LeA 35693 Foreign Countries
;  CURRENT APPLICATION NUMBER: US/10/219,051B
;  CURRENT FILING DATE:  2003-05-09
;  PRIOR APPLICATION NUMBER: US 60/312,147
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/346,382
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: US 60/333,347
;  PRIOR FILING DATE: 2001-11-26
;  NUMBER OF SEQ ID NOS: 14715
;  SOFTWARE: Perl script
; SEQ ID NO 9082
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: SWISS-Prot / P30991
;   DATABASE ENTRY DATE: 2002-06-15
US-10-219-051B-9082

  Query Match             100.0%;  Score 1830;  DB 6;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-164;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
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Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 7
US-11-371-354-68409
; Sequence 68409, Application US/11371354
; Publication No. US20060275794A1
; GENERAL INFORMATION:
;  APPLICANT: CARRINO, JOHN
;  APPLICANT:  LIANG, FENG
;  TITLE OF INVENTION: COLLECTIONS OF MATCHED BIOLOGICAL REAGENTS AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFYING MATCHED REAGENTS
;  FILE REFERENCE: INV-1005-UT2
;  CURRENT APPLICATION NUMBER: US/11/371,354
;  CURRENT FILING DATE:  2006-03-07
;  PRIOR APPLICATION NUMBER: 60/673,045
;  PRIOR FILING DATE: 2005-04-19
;  PRIOR APPLICATION NUMBER: 60/665,199
;  PRIOR FILING DATE: 2005-03-25
;  PRIOR APPLICATION NUMBER: 60/665,200
;  PRIOR FILING DATE: 2005-03-25
;  PRIOR APPLICATION NUMBER: 60/659,493
;  PRIOR FILING DATE: 2005-03-07
;  PRIOR APPLICATION NUMBER: 60/659,492
;  PRIOR FILING DATE: 2005-03-07
;  PRIOR APPLICATION NUMBER: 60/953,586
;  PRIOR FILING DATE: 2005-02-15
;  PRIOR APPLICATION NUMBER: 60/651,390
;  PRIOR FILING DATE: 2005-02-08
;  NUMBER OF SEQ ID NOS: 78682
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 68409
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-371-354-68409

  Query Match             100.0%;  Score 1830;  DB 7;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-164;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 8
US-10-545-557-19
; Sequence 19, Application US/10545557
; Publication No. US20060222654A1
; GENERAL INFORMATION:
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;  APPLICANT: ANOSYS
;  TITLE OF INVENTION: METHODS AND COMPOUNDS FOR RAISING ANTIBODIES AND FOR SCREENING ANTIBODY
;  TITLE OF INVENTION:  REPERTOIRES
;  FILE REFERENCE: 3665-158
;  CURRENT APPLICATION NUMBER: US/10/545,557
;  CURRENT FILING DATE:  2005-08-15
;  PRIOR APPLICATION NUMBER: PCT/IB2004/000888
;  PRIOR FILING DATE: 2004-02-13
;  PRIOR APPLICATION NUMBER: US60/447,291
;  PRIOR FILING DATE: 2003-02-14
;  NUMBER OF SEQ ID NOS: 86
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 363
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: CXCR4 + HA Tag
US-10-545-557-19

  Query Match             99.8%;  Score 1827;  DB 6;  Length 363;
  Best Local Similarity   99.7%;  Pred. No. 6.1e-164;
  Matches  351;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 LEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 71

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 131

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 191

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 251

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 311

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 363


RESULT 9
US-11-404-939-485
; Sequence 485, Application US/11404939
; Publication No. US20060183164A1
; GENERAL INFORMATION:
;  APPLICANT: Lehmann-Bruinsma, Karin
;  APPLICANT:  Liaw, Chen W.
;  APPLICANT:  Lin, I-Lin
;  TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Known G
;  TITLE OF INVENTION:  Protein-Coupled Receptors
;  FILE REFERENCE: AREN-207
;  CURRENT APPLICATION NUMBER: US/11/404,939
;  CURRENT FILING DATE:  2006-04-14
;  PRIOR APPLICATION NUMBER: US/09/826,509
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/195,747
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: 09/170,496
;  PRIOR FILING DATE: 1998-10-13
;  NUMBER OF SEQ ID NOS: 589
;  SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 485
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-404-939-485
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  Query Match             99.7%;  Score 1824;  DB 7;  Length 352;
  Best Local Similarity   99.7%;  Pred. No. 1.1e-163;
  Matches  351;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAKKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 10
US-10-540-898-921
; Sequence 921, Application US/10540898
; Publication No. US20060166213A1
; GENERAL INFORMATION:
;  APPLICANT: David W. Morris
;  APPLICANT:  Marc Malandro
;  TITLE OF INVENTION: Novel Compositions and Methods in Cancer
;  FILE REFERENCE: CHIR0056-101 (PP023367.0003)
;  CURRENT APPLICATION NUMBER: US/10/540,898
;  CURRENT FILING DATE:  2005-06-27
;  PRIOR APPLICATION NUMBER: US 10/330,773
;  PRIOR FILING DATE: 2002-12-27
;  NUMBER OF SEQ ID NOS: 981
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 921
;   LENGTH: 348
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-540-898-921

  Query Match             97.5%;  Score 1785;  DB 6;  Length 348;
  Best Local Similarity   98.6%;  Pred. No. 5.3e-160;
  Matches  347;  Conservative    0;  Mismatches    1;  Indels    4;  Gaps    2;

Qy          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVI 60

Qy         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVN- 119

Qy        121 YSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 -KSVLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEA 178

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 238

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
              |||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||
Db        239 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITE--AFFHCCLNPI 296

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              |||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        297 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS.348


RESULT 11
US-11-437-734-2
; Sequence 2, Application US/11437734
; Publication No. US20060211037A1
; GENERAL INFORMATION:
;  APPLICANT: KISHIMOTO, Tadamitsu
;  APPLICANT:  NAGASAWA, Takashi
;  APPLICANT:  TACHIBANA, Kazunobu
;  APPLICANT:  IIZASA, Hisashi
;  APPLICANT:  YOSHIDA, Nobuaki
;  APPLICANT:  NAKAJIMA, Toshihiro
;  APPLICANT:  YOSHIE, Osamu
;  TITLE OF INVENTION: NOVEL MOUSE CXC CHEMOKINE RECEPTOR
;  FILE REFERENCE: 1422-386P
;  CURRENT APPLICATION NUMBER: US/11/437,734
;  CURRENT FILING DATE:  2006-05-22
;  PRIOR APPLICATION NUMBER: US/09/367,052
;  PRIOR FILING DATE: 1999-08-06
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 359
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-11-437-734-2

  Query Match             91.7%;  Score 1678.5;  DB 7;  Length 359;
  Best Local Similarity   90.1%;  Pred. No. 5.9e-150;
  Matches  319;  Conservative   19;  Mismatches   11;  Indels    5;  Gaps    1;

Qy          4 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63
              :||||||||:||:||||||| |||||||:|| :||:||||||| |||||||||||||||
Db          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65

Qy         64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123
              ||||||||||||||||||||||||||||||||:|:|||| |||||||:||||||||
Db         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125

Qy        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 178
              |||||||||||||||||||||||||||||| |||||||||||||||||:|     |
Db        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185

Qy        179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 238
              : |||||||| ||: ||:||||||||||||||||||||||||||||||||||||||||
Db        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245

Qy        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 298
              |||||||||||||||||:|||||||||| :|||||:||: ||||||||||||||||||
Db        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305

Qy        299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||:|||||| |:||||||||||||||||||||||||||||||||
Db        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359


RESULT 12
US-10-219-051B-9076
; Sequence 9076, Application US/10219051B
; Publication No. US20070015145A1
; GENERAL INFORMATION:
;  APPLICANT: The General Hospital Corporation doing business as Massachusetts General
;  APPLICANT:  Hospital / Bayer AG
;  TITLE OF INVENTION: Nucleotide sequences involved in pain
;  FILE REFERENCE: LeA 35693 Foreign Countries
;  CURRENT APPLICATION NUMBER: US/10/219,051B
;  CURRENT FILING DATE:  2003-05-09
;  PRIOR APPLICATION NUMBER: US 60/312,147
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/346,382
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: US 60/333,347
;  PRIOR FILING DATE: 2001-11-26
;  NUMBER OF SEQ ID NOS: 14715
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;  SOFTWARE: Perl script
; SEQ ID NO 9076
;   LENGTH: 349
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: SWISS-Prot / O08565
;   DATABASE ENTRY DATE: 2001-10-16
US-10-219-051B-9076

  Query Match             91.4%;  Score 1673;  DB 6;  Length 349;
  Best Local Similarity   90.8%;  Pred. No. 1.9e-149;
  Matches  317;  Conservative   17;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          4 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63
              : ||||||||:||:||||||| |||||||:|| |||:||||||| |||||||||||||||
Db          1 MEIYTSDNYSEEVGSGDYDSNKEPCFRDENENFNRIFLPTIYFIIFLTGIVGNGLVILVM 60

Qy         64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123
              ||||||||||||||||||||||||||||||||||:|:|||| |||||||:|||||||||
Db         61 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 120

Qy        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEADDR 183
              |||||||||||||||||||  ||||||| |||||||||||||| |||:||: | |
Db        121 VLILAFISLDRYLAIVHATNSQSARKLLAEKAVYVGVWIPALLLTIPDIIFADVSQGDGR 180

Qy        184 YICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTVI 243
              ||||| ||: ||:||||||||||||||||||||||||||||||||||||||||||||||
Db        181 YICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTVI 240

Qy        244 LILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPILYA 303
              |||||||||||||:||||||||||:||||||||: ||||||||||||||||||||||||
Db        241 LILAFFACWLPYYVGISIDSFILLEVIKQGCEFESVVHKWISITEALAFFHCCLNPILYA 300

Qy        304 FLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              |||||||:|||||| |:|||||||||||||||||||||||||||||||
Db        301 FLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 349


RESULT 13
US-10-219-051B-9080
; Sequence 9080, Application US/10219051B
; Publication No. US20070015145A1
; GENERAL INFORMATION:
;  APPLICANT: The General Hospital Corporation doing business as Massachusetts General
;  APPLICANT:  Hospital / Bayer AG
;  TITLE OF INVENTION: Nucleotide sequences involved in pain
;  FILE REFERENCE: LeA 35693 Foreign Countries
;  CURRENT APPLICATION NUMBER: US/10/219,051B
;  CURRENT FILING DATE:  2003-05-09
;  PRIOR APPLICATION NUMBER: US 60/312,147
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/346,382
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: US 60/333,347
;  PRIOR FILING DATE: 2001-11-26
;  NUMBER OF SEQ ID NOS: 14715
;  SOFTWARE: Perl script
; SEQ ID NO 9080
;   LENGTH: 349
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: SWISS-Prot / O08565
;   DATABASE ENTRY DATE: 2001-10-16
US-10-219-051B-9080

  Query Match             91.4%;  Score 1673;  DB 6;  Length 349;
  Best Local Similarity   90.8%;  Pred. No. 1.9e-149;
  Matches  317;  Conservative   17;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          4 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63
              : ||||||||:||:||||||| |||||||:|| |||:||||||| |||||||||||||||
Db          1 MEIYTSDNYSEEVGSGDYDSNKEPCFRDENENFNRIFLPTIYFIIFLTGIVGNGLVILVM 60

Qy         64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123
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Db         61 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 120

Qy        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANVSEADDR 183
Db        121 VLILAFISLDRYLAIVHATNSQSARKLLAEKAVYVGVWIPALLLTIPDIIFADVSQGDGR 180

Qy        184 YICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTVI 243
Db        181 YICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTVI 240

Qy        244 LILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPILYA 303
Db        241 LILAFFACWLPYYVGISIDSFILLEVIKQGCEFESVVHKWISITEALAFFHCCLNPILYA 300

Qy        304 FLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
Db        301 FLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 349


RESULT 14
US-11-437-734-8
; Sequence 8, Application US/11437734
; Publication No. US20060211037A1
; GENERAL INFORMATION:
;  APPLICANT: KISHIMOTO, Tadamitsu
;  APPLICANT:  NAGASAWA, Takashi
;  APPLICANT:  TACHIBANA, Kazunobu
;  APPLICANT:  IIZASA, Hisashi
;  APPLICANT:  YOSHIDA, Nobuaki
;  APPLICANT:  NAKAJIMA, Toshihiro
;  APPLICANT:  YOSHIE, Osamu
;  TITLE OF INVENTION: NOVEL MOUSE CXC CHEMOKINE RECEPTOR
;  FILE REFERENCE: 1422-386P
;  CURRENT APPLICATION NUMBER: US/11/437,734
;  CURRENT FILING DATE:  2006-05-22
;  PRIOR APPLICATION NUMBER: US/09/367,052
;  PRIOR FILING DATE: 1999-08-06
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-11-437-734-8

  Query Match             91.3%;  Score 1671.5;  DB 7;  Length 352;
  Best Local Similarity   90.3%;  Pred. No. 2.6e-149;
  Matches  318;  Conservative   18;  Mismatches   11;  Indels    5;  Gaps    1;

Qy          6 IYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVMGY 65
Db          1 IYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVMGY 60

Qy         66 QKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSSVL 125
Db         61 QKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSSVL 120

Qy        126 ILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----SEA 180
Db        121 ILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDISQG 180

Qy        181 DDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240
Db        181 DDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        241 TVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPI 300
Db        241 TVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLNPI 300

Qy        301 LYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
Db        301 LYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 15
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US-10-540-898-918
; Sequence 918, Application US/10540898
; Publication No. US20060166213A1
; GENERAL INFORMATION:
;  APPLICANT: David W. Morris
;  APPLICANT:  Marc Malandro
;  TITLE OF INVENTION: Novel Compositions and Methods in Cancer
;  FILE REFERENCE: CHIR0056-101 (PP023367.0003)
;  CURRENT APPLICATION NUMBER: US/10/540,898
;  CURRENT FILING DATE:  2005-06-27
;  PRIOR APPLICATION NUMBER: US 10/330,773
;  PRIOR FILING DATE: 2002-12-27
;  NUMBER OF SEQ ID NOS: 981
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 918
;   LENGTH: 355
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-540-898-918

  Query Match             89.3%;  Score 1633.5;  DB 6;  Length 355;
  Best Local Similarity   88.7%;  Pred. No. 1e-145;
  Matches  314;  Conservative   19;  Mismatches   12;  Indels    9;  Gaps    3;

Qy          4 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63
              :||||||||:||:||||||| |||||:|| :||:||||||| ||||||||||||||||
Db          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65

Qy         64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123
              ||||||||||||||||||||||||||||||||:|:|||| |||||||:|||||   |
Db         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVN--KS 123

Qy        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 178
              |||||||||||||||||||||||||||||| ||||||||||||||||||:|     |
Db        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 183

Qy        179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 238
              : |||||||| ||: ||:||||||||||||||||||||||||||||||||||||||||||
Db        184 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 243

Qy        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 298
              ||||||||||||||||:|||||||||| :|||||:||: |||||||||  ||||||||
Db        244 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITE--AFFHCCLN 301

Qy        299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
              ||||||||||||:|||||| |:||||||||||||||||||||||||||||||
Db        302 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 355


Search completed: February  6, 2007, 14:31:22
Job time : 42.5963 secs
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start

SCORE 1.3 BuildDate: 11/17/2006

SCORE Search Results Details for Application 10785230 and Search Result 20070206_074015_us-10-785-230-3.rag.

This page gives you Search Results detail for the Application 10785230 and Search Result 20070206_074015_us-10-785-230-3.rag.

start | next page

Go Back to previous page

GenCore version 6.2

OM protein - protein search, using sw model

Run on: February 6, 2007, 14:07:09 ; Search time 216 Seconds
(without alignments)
814.792 Million cell updates/sec

Title: US-10-785-230-3
Perfect score: 1867
Sequence: 1 MEPISVSIYTSDNYSEEVGS.....KRGGHSSVSTESESSSFHSS 359

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200701:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*
11: geneseqp2007s:*

* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1867	100.0	359	2	AAW64778	Aaw64778 A murine
2	1867	100.0	359	2	AAY39994	Aay39994 Mouse CXC
3	1867	100.0	359	8	ADO29272	Ado29272 Mouse GPC
4	1867	100.0	359	8	ADQ97941	Adq97941 Mouse can
5	1848	99.0	357	10	AEF38898	Aef38898 Mouse che

6	1758.5	94.2	349	10	AEF38900	Aef38900 Rat chemo
7	1758.5	94.2	349	10	AEK47825	Aek47825 Rat chemo
8	1744.5	93.4	349	7	ADE63141	Ade63141 Rat Prote
9	1744.5	93.4	349	7	ADE63145	Ade63145 Rat Prote
10	1744.5	93.4	349	10	AEE66169	Aee66169 Rat CXCR4
11	1678.5	89.9	352	2	AAR68812	Aar68812 Human mon
12	1678.5	89.9	352	2	AAR80757	Aar80757 Chemokine
13	1678.5	89.9	352	2	AAY39993	Aay39993 Human CXC
14	1678.5	89.9	352	3	AAY52507	Aay52507 Human CXC
15	1678.5	89.9	352	4	AAE06690	Aae06690 Human neu
16	1678.5	89.9	352	4	AAG79088	Aag79088 Amino aci
17	1678.5	89.9	352	4	AAG80123	Aag80123 Human CXC
18	1678.5	89.9	352	5	AAO14003	Aao14003 Human cys
19	1678.5	89.9	352	5	ABP52651	Abp52651 Human CXC
20	1678.5	89.9	352	5	ABG32977	Abg32977 Human CXC
21	1678.5	89.9	352	5	ABG33065	Abg33065 Human CXC
22	1678.5	89.9	352	5	ABP65183	Abp65183 Hypoxia-r
23	1678.5	89.9	352	5	AAG78471	Aag78471 CXCR4 pro
24	1678.5	89.9	352	6	ABP96794	Abp96794 Human COP
25	1678.5	89.9	352	6	ABU03495	Abu03495 Angiogene
26	1678.5	89.9	352	6	ABR58581	Abr58581 Human can
27	1678.5	89.9	352	6	ABP97733	Abp97733 Amino aci
28	1678.5	89.9	352	6	ABP81796	Abp81796 Human CXC
29	1678.5	89.9	352	7	ADC98646	Adc98646 Human CXC
30	1678.5	89.9	352	7	ADE63147	Ade63147 Human Pro
31	1678.5	89.9	352	7	ADE63143	Ade63143 Human Pro
32	1678.5	89.9	352	7	ADF90878	Adf90878 Human hep
33	1678.5	89.9	352	7	ADO16837	Ado16837 CXCR4 ami
34	1678.5	89.9	352	7	ADN95821	Adn95821 Human BEC
35	1678.5	89.9	352	8	ADH17079	Adh17079 Human orp
36	1678.5	89.9	352	8	ADN04756	Adn04756 Antipsori
37	1678.5	89.9	352	8	ADO29271	Ado29271 Human GPC
38	1678.5	89.9	352	8	ADP12477	Adp12477 Protein e
39	1678.5	89.9	352	8	ADP12926	Adp12926 Protein e
40	1678.5	89.9	352	8	ADP13001	Adp13001 Protein e
41	1678.5	89.9	352	8	ADO19692	Ado19692 Human PRO
42	1678.5	89.9	352	8	ADO19832	Ado19832 Human PRO
43	1678.5	89.9	352	8	ADO20013	Ado20013 Human PRO
44	1678.5	89.9	352	8	ADP44055	Adp44055 Human CXC
45	1678.5	89.9	352	8	ADQ14488	Adq14488 Human che

ALIGNMENTS

RESULT 1
AAW64778
ID AAW64778 standard; protein; 359 AA.
XX
AC AAW64778;
XX
DT 20-NOV-1998 (first entry)
XX
DE A murine CXC chemokine receptor.
XX
KW Mouse; CXC chemokine receptor; pre-B cell line DW34;
KW CXC chemokine pre-B cell stimulatory factor PBSF/SDF-1; HIV infection;
KW screening; inhibitor; AIDS.
XX
OS Mus sp.
XX
PN WO9835035-A1.
XX
PD 13-AUG-1998.
XX
PF 07-FEB-1997; 97WO-JP000299.
XX
PR 07-FEB-1997; 97WO-JP000299.
XX
PA (SHIO) SHIONOGI & CO LTD.
XX
PI Kishimoto T, Nagasawa T, Tachibana K, Iizasa H, Yoshida N;
PI Nakajima T, Yoshie O;
XX
DR WPI; 1998-447232/38.
DR N-PSDB; AAV46370.

XX
PT Mouse CXC chemokine receptor binding to PBSF/SDF-1 pre-B cell stimulatory
PT factor - is useful for screening of potential HIV infection and AIDS
PT inhibitors.
XX
PS Claim 1; Page 54-56; 76pp; Japanese.
XX
CC The present sequence represents a murine CXC chemokine receptor which
CC binds to the mouse CXC chemokine pre-B cell stimulatory factor PBSF/SDF-
CC 1. The nucleic acid is isolated from mouse pre-B cell line DW34. The
CC receptor and cells expressing it can be used in the study and mapping of
CC the mechanism of HIV infection and in screening of potential inhibitors
CC of HIV infection and the development of AIDS
XX
SQ Sequence 359 AA;

Query Match 100.0%; Score 1867; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 2.1e-214;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MEPISVSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEPISVSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGL 60

Qy         61 VILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 VILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTV 120

Qy        121 NLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVS 180

Qy        181 QGDISQGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQ 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 QGDISQGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQ 240

Qy        241 KRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFF 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 KRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFF 300

Qy        301 HCCLNPILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 HCCLNPILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
```

RESULT 2
AAY39994
ID AAY39994 standard; protein; 359 AA.
XX
AC AAY39994;
XX
DT 16-DEC-1999 (first entry)
XX
DE Mouse CXCR4 protein sequence.
XX
KW CXCR4; mouse; neovascularisation; inhibitor; solid cancer; therapy;
KW tissue repairing agent; vascularisation.
XX
OS Mus sp.
XX
PN WO9948528-A1.
XX
PD 30-SEP-1999.
XX
PF 23-MAR-1999; 99WO-JP001448.
XX
PR 24-MAR-1998; 98JP-00095448.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
PA (KISH/) KISHIMOTO T.
XX
PI Kishimoto T, Nagasawa T, Tachibana K;
XX
DR WPI; 1999-591042/50.
DR N-PSDB; AAZ27611.
XX

PT CXCR4-potentiating agents and methods useful for inhibiting
PT neovascularization, and treating solid cancers.
XX
PS Disclosure; Page 49-50; 63pp; Japanese.
XX
CC This sequence is the mouse CXCR4 protein. The invention relates to
CC remedies inhibiting neovascularisation, remedies for solid cancer,
CC remedies for diseases pathologically caused by neovascularisation and
CC tissue repairing agents containing as the active ingredient a substance
CC capable of potentiating CXCR4. Based on a finding that vascularisation is
CC inhibited in a CXCR4 knockout mouse, it becomes possible to prepare
CC remedies inhibiting vascularisation which contain as the active
CC ingredient a substance capable of potentiating CXCR4, remedies for solid
CC cancer, remedies for diseases pathologically caused by neovascularisation
CC and tissue repairing agents containing as the active ingredient a
CC substance capable of potentiating CXCR4. It is also possible to establish
CC methods for treatment with the use of these remedies
XX
SQ Sequence 359 AA;

Query Match 100.0%; Score 1867; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 2.1e-214;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MEPISVSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEPISVSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGL 60

Qy         61 VILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 VILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTV 120

Qy        121 NLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVS 180

Qy        181 QGDISQGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQ 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 QGDISQGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQ 240

Qy        241 KRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFF 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 KRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFF 300

Qy        301 HCCLNPILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 HCCLNPILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
```

RESULT 3
ADO29272
ID ADO29272 standard; protein; 359 AA.
XX
AC ADO29272;
XX
DT 29-JUL-2004 (first entry)
XX
DE Mouse GPCR CXCR4, SEQ ID NO:373.
XX
KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW transgenic mouse; neurological disorder; adrenal gland disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
KW cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
KW virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;
KW dermatological; antiulcer; antithyroid; antiallergic; anorectic;
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;
KW murine; receptor.
XX
OS Mus musculus.

XX
PN WO2004040000-A2.
XX
PD 13-MAY-2004.
XX
PF 09-SEP-2003; 2003WO-US028226.
XX
PR 09-SEP-2002; 2002US-0409303P.
PR 09-APR-2003; 2003US-0461329P.
XX
PA (PRIM-) PRIMAL INC.
XX
PI Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
PI Madisen L, Mcilwain KL, Pavlova MN, Vassilatis D, Zeng H;
XX
DR WPI; 2004-390329/36.
DR N-PSDB; ADO30145.
XX
PT Novel mammalian G protein coupled receptors, useful for identifying
PT compounds that modulates diagnosing and treating disease condition
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
PT pectoris, Parkinson's disease.
XX
PS Claim 151; SEQ ID NO 373; 542pp; English.
XX
CC The invention relates to human and mouse G protein-coupled receptors
CC (GPCRs) and nucleic acids encoding them..The invention also relates to
CC sequences at least 90% identical to the GPCR proteins and nucleic acids
CC of the invention; methods of treating, preventing or diagnosing diseases
CC associated with GPCRs of the invention; methods of screening for
CC compounds useful in the treatment of GPCR-related diseases; a transgenic
CC mouse comprising a GPCR gene of the invention; a mouse comprising a
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
CC from the trasngenic mice; kits comprising several mice, each of which has
CC a mutation in a different GPCR gene of the invention; and kits comprising
CC probes which hybridise to GPCR polynucleotides of the invention. The
CC invention further discloses variants of the GPCR polypeptides and vectors
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC be used in the diagnosis, treatment or prevention of a wide variety of
CC diseases including neurological disorders (e.g., Alzheimer's disease,
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC disorders of the adrenal gland; disorders of the colon or intestine
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC myocardial infarction); muscular disorders; blood disorders (e.g.,
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
CC invention. Note: The full sequence data for this patent did not form part
CC of the printed specification; those sequences not shown were obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 359 AA;

Query Match 100.0%; Score 1867; DB 8; Length 359;
Best Local Similarity 100.0%; Pred. No. 2.1e-214;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MEPISVSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEPISVSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGL 60

Qy         61 VILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 VILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTV 120

Qy        121 NLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVS 180

Qy        181 QGDISQGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQ 240
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 QGDISQGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQ 240

Qy        241 KRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFF 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 KRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFF 300

Qy        301 HCCLNPILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 HCCLNPILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359


RESULT 4
ADQ97941
ID   ADQ97941 standard; protein; 359 AA.
XX
AC   ADQ97941;
XX
DT   07-OCT-2004  (first entry)
XX
DE   Mouse cancer associated sequence MP11-026, SEQ ID 918.
XX
KW   Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Mouse.
XX
OS   Mus musculus.
XX
PN   WO2004060304-A2.
XX
PD   22-JUL-2004.
XX
PF   22-DEC-2003; 2003WO-US041389.
XX
PR   27-DEC-2002; 2002US-00330773.
XX
PA   (SAGR-) SAGRES DISCOVERY INC.
XX
PI   Morris DW,  Malandro MS;
XX
DR   WPI; 2004-543781/52.
XX
PT   New isolated cancer associated nucleic acids comprising at least 10
PT   contiguous nucleotides, useful for diagnosing, preventing and/or treating
PT   cancers such as leukemia and lymphoma.
XX
PS   Claim 1; SEQ ID NO 918; 199pp; English.
XX
CC   The present invention relates to cancer associated sequences (ADQ97025-
CC   ADQ98004). The sequences are useful for the diagnosis, prevention and/or
CC   treatment of cancer, such as leukemia and lymphoma. Note: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic formate directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 359 AA;

  Query Match            100.0%;  Score 1867;  DB 8;  Length 359;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-214;
  Matches  359;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEPISVSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGL 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEPISVSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGL 60

Qy         61 VILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTV 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 VILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTV 120

Qy        121 NLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVS 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVS 180

Qy        181 QGDISQGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQ 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 QGDISQGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQ 240

Qy        241 KRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFF 300
```

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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 KRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFF 300

Qy        301 HCCLNPILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 HCCLNPILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359


RESULT 5
AEF38898
ID   AEF38898 standard; protein; 357 AA.
XX
AC   AEF38898;
XX
DT   23-MAR-2006  (first entry)
XX
DE   Mouse chemokine (C-X-C motif) receptor 4.
XX
KW   non-insulin dependent diabetes; antidiabetic; obesity; anorectic;
KW   insulin resistance; diagnosis.
XX
OS   Mus musculus.
XX
PN   WO2006007400-A2.
XX
PD   19-JAN-2006.
XX
PF   15-JUN-2005; 2005WO-US021297.
XX
PR   16-JUN-2004; 2004US-0580448P.
XX
PA   (META-) METABOLEX INC.
XX
PI   Moodie SA,  Zhang F,  Rack PG,  Shang J,  Lavan BE,  Allan B,  Wong C;
PI   Gregoire F,  Perez G,  Waters S;
XX
DR   WPI; 2006-110285/11.
DR   N-PSDB; AEF38897.
XX
PT   Identifying an agent for treating an obese, diabetic or pre-diabetic
PT   individual comprises selecting an agent that modulates the expression or
PT   activity of the polypeptide or that binds to the polypeptide.
XX
PS   Claim 9; SEQ ID NO 72; 281pp; English.
XX
CC   The invention relates to identifying an agent for treating an obese,
CC   diabetic or pre-diabetic individual comprises selecting an agent that
CC   modulates the expression or activity of the polypeptide or that binds to
CC   the polypeptide. The method comprises contacting an agent to a
CC   polypeptide encoded by a polynucleotide that hybridizes to a nucleic acid
CC   encoding any one the proteins included in the sequence listing (in 50%
CC   formamide, 5 x SSC, and 1% SDS at 42 degrees C followed by a wash in 0.2
CC   x SSC, and 0.1% SDS at 55 degrees C) and selecting an agent that
CC   modulates the expression or activity of the polypeptide, or that binds to
CC   the polypeptide, thus identifying an agent for treating an obese,
CC   diabetic or pre-diabetic individual. The method further comprises
CC   detecting whether the selected agent modulates weight and/or obesity, or
CC   insulin sensitivity. The polypeptide is expressed in a cell and the cell
CC   is contacted with the agent. The method is useful for identifying an
CC   agent for treating obesity or diabetes. The present sequence represents a
CC   full length mouse polypeptide of the invention.
XX
SQ   Sequence 357 AA;

  Query Match          99.0%;  Score 1848;  DB 10;  Length 357;
  Best Local Similarity   99.4%;  Pred. No. 3.9e-212;
  Matches  357;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    1;

Qy          1 MEPISVSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGL 60
              ||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEPI--SIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGL 58

Qy         61 VILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         59 VILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTV 118
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Qy        121 NLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 NLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVS 178

Qy        181 QGDISQGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQ 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 QGDISQGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQ 238

Qy        241 KRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFF 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 KRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFF 298

Qy        301 HCCLNPILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        299 HCCLNPILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 357
```

RESULT 6
AEF38900
ID AEF38900 standard; protein; 349 AA.
XX
AC AEF38900;
XX
DT 23-MAR-2006 (first entry)
XX
DE Rat chemokine (C-X-C motif) receptor 4.
XX
KW non-insulin dependent diabetes; antidiabetic; obesity; anorectic;
KW insulin resistance; diagnosis.
XX
OS Rattus norvegicus.
XX
PN WO2006007400-A2.
XX
PD 19-JAN-2006.
XX
PF 15-JUN-2005; 2005WO-US021297.
XX
PR 16-JUN-2004; 2004US-0580448P.
XX
PA (META-) METABOLEX INC.
XX
PI Moodie SA, Zhang F, Rack PG, Shang J, Lavan BE, Allan B, Wong C;
PI Gregoire F, Perez G, Waters S;
XX
DR WPI; 2006-110285/11.
DR N-PSDB; AEF38899.
XX
PT Identifying an agent for treating an obese, diabetic or pre-diabetic
PT individual comprises selecting an agent that modulates the expression or
PT activity of the polypeptide or that binds to the polypeptide.
XX
PS Claim 9; SEQ ID NO 74; 281pp; English.
XX
CC The invention relates to identifying an agent for treating an obese,
CC diabetic or pre-diabetic individual comprises selecting an agent that
CC modulates the expression or activity of the polypeptide or that binds to
CC the polypeptide. The method comprises contacting an agent to a
CC polypeptide encoded by a polynucleotide that hybridizes to a nucleic acid
CC encoding any one the proteins included in the sequence listing (in 50%
CC formamide, 5 x SSC, and 1% SDS at 42 degrees C followed by a wash in 0.2
CC x SSC, and 0.1% SDS at 55 degrees C) and selecting an agent that
CC modulates the expression or activity of the polypeptide, or that binds to
CC the polypeptide, thus identifying an agent for treating an obese,
CC diabetic or pre-diabetic individual. The method further comprises
CC detecting whether the selected agent modulates weight and/or obesity, or
CC insulin sensitivity. The polypeptide is expressed in a cell and the cell
CC is contacted with the agent. The method is useful for identifying an
CC agent for treating obesity or diabetes. The present sequence represents a
CC full length rat polypeptide of the invention.
XX
SQ Sequence 349 AA;

```
  Query Match             94.2%;  Score 1758.5;  DB 10;  Length 349;
  Best Local Similarity   96.0%;  Pred. No. 2.1e-201;
  Matches  340;  Conservative    4;  Mismatches    5;  Indels    5;  Gaps    1;
```

```
Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              : |||||||||||||||||||||||||||| :|||||||||||||||||||||||||||||
Db          1 MEIYTSDNYSEEVGSGDYDSNKEPCFRDENENFNRIFLPTIYFIIFLTGIVGNGLVILVM 60

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 120

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||     |
Db        121 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDIIFADV-----S 175

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 QGDGRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 235

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
              |||||||||||||||||||||||||| ||||||:|||:||||||||||||||||||||||
Db        236 KTTVILILAFFACWLPYYVGISIDSFILLEVIKQGCEFESVVHKWISITEALAFFHCCLN 295

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 349
```

RESULT 7
AEK47825
ID   AEK47825 standard; protein; 349 AA.
XX
AC   AEK47825;
XX
DT   16-NOV-2006 (first entry)
XX
DE   Rat chemokine (C-X-C motif) receptor 4.
XX
KW   Lipidosis; antilipemic; neurological disease; diagnosis; gene expression;
KW   chemokine (C-X-C motif) receptor 4.
XX
OS   Rattus norvegicus.
XX
PN   WO2006088226-A1.
XX
PD   24-AUG-2006.
XX
PF   16-FEB-2006; 2006WO-JP303205.
XX
PR   17-FEB-2005; 2005JP-00040698.
PR   26-APR-2005; 2005JP-00128412.
XX
PA   (TAKE) TAKEDA PHARM CO LTD.
XX
PI   Sawada H, Mori I, Takami K;
XX
DR   WPI; 2006-669225/69.
DR   N-PSDB; AEK47824.
XX
PT   Reagent useful for determining phospholipidosis in mammal, comprises
PT   nucleic acid capable of hybridizing to nucleic acid being a
PT   phospholipidosis marker gene such as ATX1, CXCR4, Fbx15 and PRA1.
XX
PS   Disclosure; SEQ ID NO 77; 177pp; Japanese.
XX
CC   The invention relates to a reagent for determining phospholipidosis in a
CC   mammal, comprises a nucleic acid (N1) capable of hybridizing under high
CC   stringent conditions to a nucleic acid given in the specification, and/or
CC   a nucleic acid capable of hybridizing under high stringent conditions
CC   with the nucleic acid having a base sequence complementary to (N1). Also
CC   included are a kit for determining phospholipidosis in a mammal
CC   (comprising the reagents as cited, or the reagents including the nucleic
CC   acid capable of hybridizing under high stringent conditions with the
CC   transcription product of the gene whose expression fluctuates in
CC   correlation to the phospholipidosis disease onset, and/or nucleic acid
CC   capable of hybridizing under high stringent conditions with a nucleic
CC   acid having a base sequence complementary to the transcript product, so
CC   as to enable detection of the expression of the gene) and determining

CC phospholipidosis disease in a mammal (comprising detecting expression
CC fluctuation of one or more genes, being correlated to the onset of the
CC phospholipidosis disease, in a sample collected from a mammal, where at
CC least one gene has a base sequence that is the same or substantially same
CC as a nucleic acid given in the specification). The nucleic acid sequences
CC are useful for determining phospholipidosis disease in a mammal (such as
CC human, rat, mouse, dog or monkey), using a sample such as blood or
CC lymphocyte, where the phospholipidosis disease originates from a compound
CC or the mammal had administered or exposed to the compound, and the
CC compound has cationic amphiphilic drug structure. The reagent enables
CC rapid, simple and precise or non-invasive determination of
CC phospholipidosis disease in a mammal, with decreased appearance frequency
CC of false-positive results. The present sequence represents a protein
CC encoded by a rat cDNA a change in expression of which correlates with
CC onset of phospholipidosis.
XX
SQ Sequence 349 AA;

Query Match 94.2%; Score 1758.5; DB 10; Length 349;
Best Local Similarity 96.0%; Pred. No. 2.1e-201;
Matches 340; Conservative 4; Mismatches 5; Indels 5; Gaps 1;

```
Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              : |||||||||||||||||||||||||||| :|||||||||||||||||||||||||||
Db          1 MEIYTSDNYSEEVGSGDYDSNKEPCFRDENENFNRIFLPTIYFIIFLTGIVGNGLVILVM 60

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 120

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||||||||||||||||||||||||||||| |||||     |
Db        121 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDIIFADV-----S 175

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 QGDGRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 235

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
              |||||||||||||||||||||||||||| ||||||:|||:||||||||||||||||||||
Db        236 KTTVILILAFFACWLPYYVGISIDSFILLEVIKQGCEFESVVHKWISITEALAFFHCCLN 295

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 349
```

RESULT 8
ADE63141
ID ADE63141 standard; protein; 349 AA.
XX
AC ADE63141;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein O08565, SEQ ID NO 9076.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;

XX
DR WPI; 2003-268312/26.
DR GENBANK; O08565.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 349 AA;

Query Match 93.4%; Score 1744.5; DB 7; Length 349;
Best Local Similarity 95.5%; Pred. No. 9.9e-200;
Matches 338; Conservative 4; Mismatches 7; Indels 5; Gaps 1;

```
Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              : ||||||||||||||||||||||||||| :|||||||||||||||||||||||||||
Db          1 MEIYTSDNYSEEVGSGDYDSNKEPCFRDENENFNRIFLPTIYFIIFLTGIVGNGLVILVM 60

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 120

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||  |||||||||||||||||||||| |||||     |
Db        121 VLILAFISLDRYLAIVHATNSQSARKLLAEKAVYVGVWIPALLLTIPDIIFADV-----S 175

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 QGDGRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 235

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
              |||||||||||||||||||||||||||| |||||:|||:|||||||||||||||||||
Db        236 KTTVILILAFFACWLPYYVGISIDSFILLEVIKQGCEFESVVHKWISITEALAFFHCCLN 295

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 349
```

RESULT 9
ADE63145
ID ADE63145 standard; protein; 349 AA.
XX
AC ADE63145;
XX
DT 29-JAN-2004 (first entry)
XX

DE Rat Protein O08565, SEQ ID NO 9080.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; O08565.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 349 AA;

Query Match 93.4%; Score 1744.5; DB 7; Length 349;
Best Local Similarity 95.5%; Pred. No. 9.9e-200;
Matches 338; Conservative 4; Mismatches 7; Indels 5; Gaps 1;

```
Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              : |||||||||||||||||||||||||| :|||||||||||||||||||||||||
Db          1 MEIYTSDNYSEEVGSGDYDSNKEPCFRDENENFNRIFLPTIYFIIFLTGIVGNGLVILVM 60

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 120

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||  |||||||||||||||||||||| |||||     |
Db        121 VLILAFISLDRYLAIVHATNSQSARKLLAEKAVYVGVWIPALLLTIPDIIFADV-----S 175
```

```
Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 QGDGRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 235

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
              |||||||||||||||||||||||||||| |||||:|||:||||||||||||||||||||
Db        236 KTTVILILAFFACWLPYYVGISIDSFILLEVIKQGCEFESVVHKWISITEALAFFHCCLN 295

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 349
```

RESULT 10
AEE66169
ID   AEE66169 standard; protein; 349 AA.
XX
AC   AEE66169;
XX
DT   09-FEB-2006 (first entry)
XX
DE   Rat CXCR4, SEQ ID 2.
XX
KW   Cardiant; Cell therapy; stem cell; myocardial infarction;
KW   CXC chemokine receptor 4.
XX
OS   Rattus norvegicus.
XX
PN   US2005271639-A1.
XX
PD   08-DEC-2005.
XX
PF   04-JAN-2005; 2005US-00028922.
XX
PR   22-AUG-2002; 2002US-0405274P.
PR   30-APR-2003; 2003US-00426712.
PR   19-MAY-2004; 2004US-0572349P.
XX
PA   (PENN/) PENN M S.
PA   (KIED/) KIEDROWSKI M.
XX
PI   Penn MS, Kiedrowski M;
XX
DR   WPI; 2006-018799/02.
DR   N-PSDB; AEE66171.
DR   SWISSPROT; O08565.
XX
PT   New isolated stem cell genetically modified to express at least one of
PT   CXC chemokine receptor 4 (CXCR4), SDF-1, or its variant, useful for
PT   treating myocardial infarction.
XX
PS   Claim 2; SEQ ID NO 2; 27pp; English.
XX
CC   The present invention relates to a novel isolated stem cell genetically
CC   modified to express at least one of CXC chemokine receptor 4 (CXCR4),
CC   stromal cell-derived factor-1 (SDF-1), or its variant thereof. The stem
CC   cell is useful for treating myocardial infarction. CXCR4, also known as
CC   CD184, leukocyte-derived seven transmembrane domain receptor (LESTR),
CC   neuropeptide Y receptor Y3 (NPY3R), HM89 and FB22, is a G protein-coupled
CC   receptor with selectivity for the chemokine SDF-1. CXCR4 mediates
CC   chemotaxis in mature and progenitor blood cells and, together with its
CC   ligand SDF-1, is essential for B lympho- and myelopoiesis. In addition to
CC   hematopoiesis, CXCR4 is responsible for cardiac ventricular septum
CC   formation, vascularization of the gastrointestinal tract and development
CC   of cerebellar granule cells. The present sequence is a CXCR4, which was
CC   used to illustrate the invention.
XX
SQ   Sequence 349 AA;

```
  Query Match             93.4%;  Score 1744.5;  DB 10;  Length 349;
  Best Local Similarity   95.5%;  Pred. No. 9.9e-200;
  Matches  338;  Conservative    4;  Mismatches    7;  Indels    5;  Gaps    1;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              : |||||||||||||||||||||||||||| :||||||||||||||||||||||||||||
Db          1 MEIYTSDNYSEEVGSGDYDSNKEPCFRDENENFNRIFLPTIYFIIFLTGIVGNGLVILVM 60
```

```
Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 120

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||||  ||||||||||||||||||||||| |||||     |
Db        121 VLILAFISLDRYLAIVHATNSQSARKLLAEKAVYVGVWIPALLLTIPDIIFADV-----S 175

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 QGDGRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 235

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
              |||||||||||||||||||||||||||| ||||||:|||:|||||||||||||||||||
Db        236 KTTVILILAFFACWLPYYVGISIDSFILLEVIKQGCEFESVVHKWISITEALAFFHCCLN 295

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 349
```

```
RESULT 11
AAR68812
ID   AAR68812 standard; protein; 352 AA.
XX
AC   AAR68812;
XX
DT   25-MAR-2003  (revised)
DT   18-JUL-1995  (first entry)
XX
DE   Human monocyte PF4AR.
```

start | next page

SCORE 1.3 BuildDate: 11/17/2006

SCORE Search Results Details for Application 10785230 and Search Result 20070206_074020_us-10-785-230-3.rup.

This page gives you Search Results detail for the Application 10785230 and Search Result 20070206_074020_us-10-785-230-3.rup.

start | next page

Go Back to previous page

GenCore version 6.2

OM protein - protein search, using sw model

Run on: February 6, 2007, 14:08:15 ; Search time 232 Seconds
(without alignments)
1660.742 Million cell updates/sec

Title: US-10-785-230-3
Perfect score: 1867
Sequence: 1 MEPISVSIYTSDNYSEEVGS.....KRGGHSSVSTESESSSFHSS 359

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_8.4:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1867	100.0	359	1	CXCR4_MOUSE	P70658 m c-x-c che
2	1758.5	94.2	349	2	Q8VD47_RAT	Q8vd47 rattus norv
3	1744.5	93.4	349	1	CXCR4_RAT	O08565 rattus norv
4	1692.5	90.7	352	2	Q7YS92_9EUTH	Q7ys92 tupaia chin
5	1691.5	90.6	352	2	Q8HZU1_CALJA	Q8hzu1 callithrix
6	1689.5	90.5	352	2	Q8HZU0_SAISC	Q8hzu0 saimiri sci
7	1686.5	90.3	352	1	CXCR4_PAPAN	P56491 papio anubi
8	1679.5	90.0	352	1	CXCR4_MACFA	Q28474 macaca fasc
9	1679.5	90.0	352	2	O77488_CERAE	O77488 cercopithec
10	1678.5	89.9	347	2	Q9MZM9_ATEPA	Q9mzm9 ateles pani
11	1678.5	89.9	352	1	CXCR4_HUMAN	P61073 homo sapien
12	1678.5	89.9	352	1	CXCR4_PANTR	P61072 pan troglod
13	1678.5	89.9	352	2	Q53S69_HUMAN	Q53s69 homo sapien
14	1677.5	89.9	347	2	Q9MZP7_9PRIM	Q9mzp7 presbytis s

15	1676.5	89.8	347	2	Q9MZP5_9PRIM	Q9mzp5 presbytis p
16	1676.5	89.8	347	2	Q9MZP8_COLPO	Q9mzp8 colobus pol
17	1676.5	89.8	347	2	Q9MZQ2_PYGRO	Q9mzq2 pygathrix r
18	1676.5	89.8	347	2	Q9MZQ1_PYGBI	Q9mzq1 pygathrix b
19	1676.5	89.8	347	2	Q9MZP0_MACAS	Q9mzp0 macaca assa
20	1676.5	89.8	347	2	Q9MZM5_PITPI	Q9mzm5 pithecia pi
21	1676.5	89.8	347	2	Q9MZN8_MACTH	Q9mzn8 macaca thib
22	1676.5	89.8	347	2	Q9MZN7_MACNE	Q9mzn7 macaca neme
23	1676.5	89.8	347	2	Q9MZP9_NASLA	Q9mzp9 nasalis lar
24	1676.5	89.8	347	2	Q9MZQ3_PYGAV	Q9mzq3 pygathrix a
25	1676.5	89.8	347	2	Q9MZQ0_PYGNE	Q9mzq0 pygathrix n
26	1676.5	89.8	347	2	Q9MZP4_PREFR	Q9mzp4 presbytis f
27	1676.5	89.8	347	2	Q9MZN9_MACAR	Q9mzn9 macaca arct
28	1676.5	89.8	347	2	Q9MZM7_CALGO	Q9mzm7 callimico g
29	1676.5	89.8	352	1	CXCR4_MACMU	P79394 macaca mula
30	1676.5	89.8	352	2	Q9TSQ8_CERAE	Q9tsq8 cercopithec
31	1674.5	89.7	347	2	Q9MZM1_EULMA	Q9mzm1 eulemur mac
32	1674.5	89.7	347	2	Q9MZN0_ALOSE	Q9mzn0 alouatta se
33	1672.5	89.6	347	2	Q9MZP2_MANSP	Q9mzp2 mandrillus
34	1672.5	89.6	352	2	Q9BDS5_MACFA	Q9bds5 macaca fasc
35	1671.5	89.5	347	2	Q9MZN4_HYLLA	Q9mzn4 hylobates l
36	1670.5	89.5	347	2	Q9MZN2_PONPY	Q9mzn2 pongo pygma
37	1670.5	89.5	347	2	Q9MZN1_9PRIM	Q9mzn1 gorilla gor
38	1670.5	89.5	347	2	Q9MZN6_HYLLE	Q9mzn6 nomascus le
39	1670.5	89.5	347	2	Q9MZN5_BUNHO	Q9mzn5 bunopithecu
40	1670.5	89.5	352	2	Q9BXA0_HUMAN	Q9bxa0 homo sapien
41	1668.5	89.4	347	2	Q9MZP6_9PRIM	Q9mzp6 presbytis j
42	1668.5	89.4	347	2	Q9MZM6_CALMO	Q9mzm6 callicebus
43	1668.5	89.4	347	2	Q9MZP3_SEMEN	Q9mzp3 semnopithec
44	1668.5	89.4	352	1	CXCR4_CERTO	O62747 cercocebus
45	1665.5	89.2	347	2	Q9MZN3_HYLSY	Q9mzn3 hylobates s

ALIGNMENTS

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RESULT 1
CXCR4_MOUSE
ID   CXCR4_MOUSE     STANDARD;      PRT;   359 AA.
AC   P70658; O09059; O09062; P70233; P70346; Q4KMW1;
DT   01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
DT   01-NOV-1997, sequence version 2.
DT   13-JUN-2006, entry version 58.
DE   C-X-C chemokine receptor type 4 (CXC-R4) (CXCR-4) (Stromal cell-
DE   derived factor 1 receptor) (SDF-1 receptor) (Fusin) (Leukocyte-derived
DE   seven transmembrane domain receptor) (LESTR) (Pre-B-cell-derived
DE   chemokine receptor) (PB-CKR) (CD184 antigen).
GN   Name=Cxcr4; Synonyms=Cmkar4, Lestr, Sdf1r;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE (ISOFORM CXCR4-B).
RC   STRAIN=129/Sv, and C57BL/6J; TISSUE=Peritoneal exudate;
RX   MEDLINE=97113334; PubMed=8955194;
RA   Heesen M., Berman M.A., Benson J.D., Gerard C., Dorf M.E.;
RT   "Cloning of the mouse fusin gene, homologue to a human HIV-1 co-
RT   factor.";
RL   J. Immunol. 157:5455-5460(1996).
RN   [2]
RP   NUCLEOTIDE SEQUENCE (ISOFORM CXCR4-B).
RC   TISSUE=Pre-B cell;
RX   MEDLINE=97121456; PubMed=8962122; DOI=10.1073/pnas.93.25.14726;
RA   Nagasawa T., Nakajima T., Tachibana K., Iizasa H., Bleul C.C.,
RA   Yoshie O., Matsushima K., Yoshida N., Springer T.A., Kishimoto T.;
RT   "Molecular cloning and characterization of a murine pre-B-cell growth-
RT   stimulating factor/stromal cell-derived factor 1 receptor, a murine
RT   homolog of the human immunodeficiency virus 1 entry coreceptor
RT   fusin.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:14726-14729(1996).
RN   [3]
RP   NUCLEOTIDE SEQUENCE (ISOFORM CXCR4-B).
RC   STRAIN=129/Sv; TISSUE=Thymus;
RA   Schubel A., Burgstahler R., Lipp M.;
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RL Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE (ISOFORMS CXCR4-A AND CXCR4-B).
RC STRAIN=C57BL/6J X CBA; TISSUE=Thymus;
RX MEDLINE=97439495; PubMed=9295051;
RA Moepps B., Frodl R., Rodewald H.-R., Baggiolini M., Gierschik P.;
RT "Two murine homologues of the human chemokine receptor CXCR4 mediating
RT stromal cell-derived factor lalpha activation of Gi2 are
RT differentially expressed in vivo.";
RL Eur. J. Immunol. 27:2102-2112(1997).
RN [5]
RP NUCLEOTIDE SEQUENCE (ISOFORMS CXCR4-A AND CXCR4-B).
RX MEDLINE=97256574; PubMed=9103415;
RA Heesen M., Berman M.A., Hoepken U.E., Gerard N.P., Dorf M.E.;
RT "Alternate splicing of mouse fusin/CXC chemokine receptor-4: stromal
RT cell-derived factor-1alpha is a ligand for both CXC chemokine
RT receptor-4 isoforms.";
RL J. Immunol. 158:3561-3564(1997).
RN [6]
RP NUCLEOTIDE SEQUENCE (ISOFORM CXCR4-B).
RC STRAIN=C57BL/6; TISSUE=Thymus;
RA Suzuki G., Nakata Y., Uzawa A., Shirasawa T., Saito T., Mita K.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM CXCR4-B).
RC STRAIN=FVB/N; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP ALTERNATIVE SPLICING.
RX MEDLINE=99095114; PubMed=9879064;
RA Frodl R., Gierschik P., Moepps B.;
RT "Genomic organization and expression of the CXCR4 gene in mouse and
RT man: absence of a splice variant corresponding to mouse CXCR4-B in
RT human tissues.";
RL J. Recept. Signal Transduct. Res. 18:321-344(1998).
RN [9]
RP FUNCTION.
RX MEDLINE=98295994; PubMed=9634237; DOI=10.1038/31261;
RA Tachibana K., Hirota S., Iizasa H., Yoshida H., Kawabata K.,
RA Kataoka Y., Kitamura Y., Matsushima K., Yoshida N., Nishikawa S.,
RA Kishimoto T., Nagasawa T.;
RT "The chemokine receptor CXCR4 is essential for vascularization of the
RT gastrointestinal tract.";
RL Nature 393:591-594(1998).
RN [10]
RP FUNCTION.
RX MEDLINE=98295995; PubMed=9634238; DOI=10.1038/31269;
RA Zou Y.-R., Kottmann A.H., Kuroda M., Taniuchi I., Littman D.R.;
RT "Function of the chemokine receptor CXCR4 in haematopoiesis and in
RT cerebellar development.";
RL Nature 393:595-599(1998).
RN [11]
RP DEVELOPMENTAL STAGE.
RC STRAIN=ICR;
RX MEDLINE=99410349; PubMed=10479460; DOI=10.1006/dbio.1999.9405;
RA McGrath K.E., Koniski A.D., Maltby K.M., McGann J.K., Palis J.;

```
RT   "Embryonic expression and function of the chemokine SDF-1 and its
RT   receptor, CXCR4.";
RL   Dev. Biol. 213:442-456(1999).
CC   -!- FUNCTION: Receptor for the C-X-C chemokine CXCL12/SDF-1.
CC       Transduces a signal by increasing the intracellular calcium ions
CC       level. Involved in B-cell lymphopoiesis, bone-marrow myelopoiesis
CC       and in cardiac ventricular septum formation. Plays also an
CC       essential role in vascularization of the gastrointestinal tract,
CC       probably by regulating vascular branching and/or remodelling
CC       processes in endothelial cells. Involved in cerebellar neuronal
CC       layer formation, preventing premature migration of proliferating
CC       granule cells from the external granule layer inwards. In the CNS,
CC       could mediate hippocampal-neuron survival.
CC   -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=CXCR4-B; Synonyms=LESTR-B;
CC         IsoId=P70658-1; Sequence=Displayed;
CC       Name=CXCR4-A; Synonyms=LESTR-A;
CC         IsoId=P70658-2; Sequence=VSP_001891;
CC   -!- TISSUE SPECIFICITY: Lymphocytes, macrophages, neutrophils,
CC       microglial cells and astrocytes. Found in spleen, thymus, bone
CC       marrow, lymph nodes and, at lower levels in brain, small
CC       intestine, stomach and kidney. CXCR4-A is predominant in all
CC       tissues tested.
CC   -!- DEVELOPMENTAL STAGE: High expression during embryonic development
CC       does not seem to be associated with the differentiation of any
CC       particular cell type, but is widely utilized when there is a
CC       requirement for cell movement. Frequently associated with less
CC       differentiated cell types and down-regulated with subsequent
CC       differentiation. Detected in sites with haemopoietic potential:
CC       the yolk sac (7.5, 8.5 and 12.5 dpc) and fetal liver (12.5 dpc).
CC       During gastrulation, at 7.2 to 7.8 dpc, expressed in the mesoderm
CC       and the definitive endoderm. As gastrulation pattern fades (8.5
CC       dpc), expression in the mesoderm is down-regulated, while it
CC       becomes predominant in neural ectoderm. Endodermal expression is
CC       retained in the foregut and later in a subset of foregut
CC       derivatives, including the stomach (10.5 dpc), the cystic ducts of
CC       the gall bladder and the lung epithelium (12.5 dpc). In neuronal
CC       tissue: at 10.5 and 12.5 dpc, expressed in the dorsal root
CC       ganglia, in the ventral mantle layer of the spinal cord (or basal
CC       plates), in the hindbrain. At 14.5 dpc, expression more tightly
CC       confined to the neural epithelium lining the ventricular space and
CC       to the external granular layer of the ventral rhombic lip (the
CC       developing cerebellum). Expressed in the outpocketing of the
CC       diencephalic floor at 10.5 dpc and in the developing thalamus and,
CC       to a lesser extent, the developing hypothalamus. At 14.5 dpc,
CC       restricted to the region where thalamus and hypothalamus meet.
CC       Detected in a discrete band of cells at the edge of the olfactory
CC       bulb. In the vascular system: expressed in the endothelium of
CC       numerous blood vessels, but not all, at 10.5, 11.5 and 12.5 dpc,
CC       such as vitelline/umbilical vessels, cardiac ventricular wall
CC       capillaries, facial vessels and, at 14.5 pdc, in the vasculature
CC       of the herniated gut. Expression seems to be associated with
CC       expanding vascular networks. In the heart development, expressed
CC       at 10.5 dpc in the precursor to the aortopulmonary (AP) septum. At
CC       12.5 dpc, detected in the AP septum at the base of the outflow
CC       tract and in the atrioventricular valves. Detected in cranofacial
CC       ectoderm from 10.5 to 14.5 dpc. At 10.5 and 11.5 dpc, expressed in
CC       the Rathke pouch.
CC   -!- PTM: Sulfated (By similarity).
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; U59760; AAB07725.1; -; mRNA.
DR   EMBL; U65580; AAC52953.1; -; Genomic_DNA.
DR   EMBL; D87747; BAA13451.1; -; mRNA.
DR   EMBL; Z80111; CAB02201.1; -; mRNA.
DR   EMBL; Z80112; CAB02202.1; -; mRNA.
DR   EMBL; X99581; CAA67893.1; -; Genomic_DNA.
DR   EMBL; X99582; CAA67894.1; -; mRNA.
DR   EMBL; AB000803; BAA19187.1; -; mRNA.
DR   EMBL; BC031665; AAH31665.1; -; mRNA.
DR   EMBL; BC098322; AAH98322.1; -; mRNA.
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DR   UniGene; Mm.1401; -.
DR   Ensembl; ENSMUSG00000045382; Mus musculus.
DR   MGI; MGI:109563; Cxcr4.
DR   GO; GO:0030426; C:growth cone; IDA.
DR   GO; GO:0001667; P:ameboidal cell migration; IMP.
DR   GO; GO:0007420; P:brain development; IMP.
DR   GO; GO:0007281; P:germ cell development; IMP.
DR   GO; GO:0008354; P:germ cell migration; IMP.
DR   GO; GO:0008045; P:motor axon guidance; IMP.
DR   GO; GO:0001764; P:neuron migration; IDA.

  Query Match             100.0%;  Score 1867;  DB 1;  Length 359;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-137;
  Matches  359;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEPISVSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGL 60
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Db          1 MEPISVSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGL 60

Qy         61 VILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 VILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTV 120

Qy        121 NLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVS 180

Qy        181 QGDISQGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQ 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 QGDISQGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQ 240

Qy        241 KRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFF 300
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Db        241 KRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFF 300

Qy        301 HCCLNPILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
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Db        301 HCCLNPILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359


RESULT 2
Q8VD47_RAT
ID   Q8VD47_RAT     PRELIMINARY;   PRT;   349 AA.
AC   Q8VD47;
DT   01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2002, sequence version 1.
DT   04-APR-2006, entry version 27.
DE   Chemokine receptor CXCR4 (CXC chemokine receptor).
GN   Name=Cxcr4;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Holtzman; TISSUE=Whole brain;
RA   Simen A.A., Miller R.J.;
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RA   Director MGC Project;
RL   Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Membrane (By similarity).
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AF452185; AAL47855.1; -; mRNA.
DR   EMBL; BC089804; AAH89804.1; -; mRNA.
DR   UniGene; Rn.44431; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR   GO; GO:0016494; F:C-X-C chemokine receptor activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR000355; Chmkine_rcpt.
DR   InterPro; IPR001277; CXC_4_rcpt.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00657; CCCHEMOKINER.
DR   PRINTS; PR00645; CXCCHMKINER4.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Membrane; Receptor; Transducer;
KW   Transmembrane.
SQ   SEQUENCE   349 AA;  39429 MW;  09D19860D3D2CB8A CRC64;

  Query Match             94.2%;  Score 1758.5;  DB 2;  Length 349;
  Best Local Similarity   96.0%;  Pred. No. 4.7e-129;
  Matches  340;  Conservative    4;  Mismatches    5;  Indels    5;  Gaps    1;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
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Db          1 MEIYTSDNYSEEVGSGDYDSNKEPCFRDENENFNRIFLPTIYFIIFLTGIVGNGLVILVM 60

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 120

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||||||||||||||||||||||||||||| |||||     |
Db        121 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDIIFADV-----S 175

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 QGDGRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 235

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
              |||||||||||||||||||||||||| |||||:|||:||||||||||||||||||||
Db        236 KTTVILILAFFACWLPYYVGISIDSFILLEVIKQGCEFESVVHKWISITEALAFFHCCLN 295

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 349


RESULT 3
CXCR4_RAT
ID   CXCR4_RAT      STANDARD;      PRT;   349 AA.
AC   O08565;
DT   01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
```

```
DT   01-JUL-1997, sequence version 1.
DT   27-JUN-2006, entry version 44.
DE   C-X-C chemokine receptor type 4 (CXC-R4) (CXCR-4) (Stromal cell-
DE   derived factor 1 receptor) (SDF-1 receptor) (Fusin) (Leukocyte-derived
DE   seven transmembrane domain receptor) (LESTR) (CD184 antigen).
GN   Name=Cxcr4; Synonyms=Cmkar4;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   STRAIN=Wistar; TISSUE=Spleen;
RA   Harrison J.K., Salafranca M.N.;
RT   "Molecular cloning of rat CXCR4.";
RL   Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor for the C-X-C chemokine CXCL12/SDF-1.
CC       Transduces a signal by increasing the intracellular calcium ions
CC       level. Involved in B-cell lymphopoiesis, bone-marrow myelopoiesis
CC       and in cardiac ventricular septum formation. Plays also an
CC       essential role in vascularization of the gastrointestinal tract,
CC       probably by regulating vascular branching and/or remodelling
CC       processes in endothelial cells. Involved in cerebellar neuronal
CC       layer formation, preventing premature migration of proliferating
CC       granule cells from the external granule layer inwards. In the CNS,
CC       could mediate hippocampal-neuron survival (By similarity).
CC   -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
CC   -!- TISSUE SPECIFICITY: Expressed in neurons and in astrocytes.
CC   -!- PTM: Sulfated (By similarity).
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; U90610; AAB50408.1; -; mRNA.
DR   Ensembl; ENSRNOG00000003866; Rattus norvegicus.
DR   RGD; 620465; Cxcr4.
DR   GO; GO:0016494; F:C-X-C chemokine receptor activity; TAS.
DR   GO; GO:0001764; P:neuron migration; IDA.
DR   GO; GO:0008038; P:neuron recognition; IEP.
DR   InterPro; IPR000355; Chmkine_rcpt.
DR   InterPro; IPR001277; CXC_4_rcpt.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00657; CCCHEMOKINER.
DR   PRINTS; PR00645; CXCCHMKINER4.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Membrane; Receptor;
KW   Sulfation; Transducer; Transmembrane.
FT   CHAIN         1    349       C-X-C chemokine receptor type 4.
FT                                /FTId=PRO_0000069358.
FT   TOPO_DOM      1     36       Extracellular (Potential).
FT   TRANSMEM     37     60       1 (Potential).
FT   TOPO_DOM     61     76       Cytoplasmic (Potential).
FT   TRANSMEM     77     96       2 (Potential).
FT   TOPO_DOM     97    107       Extracellular (Potential).
FT   TRANSMEM    108    129       3 (Potential).
FT   TOPO_DOM    130    151       Cytoplasmic (Potential).
FT   TRANSMEM    152    172       4 (Potential).
FT   TOPO_DOM    173    197       Extracellular (Potential).
FT   TRANSMEM    198    217       5 (Potential).
FT   TOPO_DOM    218    237       Cytoplasmic (Potential).
FT   TRANSMEM    238    258       6 (Potential).
FT   TOPO_DOM    259    282       Extracellular (Potential).
FT   TRANSMEM    283    302       7 (Potential).
FT   TOPO_DOM    303    349       Cytoplasmic (Potential).
FT   MOD_RES       4      4       Sulfotyrosine (Potential).
FT   MOD_RES      18     18       Sulfotyrosine (Potential).
FT   CARBOHYD      8      8       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    106    183       By similarity.
SQ   SEQUENCE   349 AA;  39334 MW;  7E0789A605C60C09 CRC64;

  Query Match             93.4%;  Score 1744.5;  DB 1;  Length 349;
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  Best Local Similarity   95.5%;  Pred. No. 5.8e-128;
  Matches  338;  Conservative    4;  Mismatches    7;  Indels    5;  Gaps    1;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              : |||||||||||||||||||||||||| :|||||||||||||||||||||||||||
Db          1 MEIYTSDNYSEEVGSGDYDSNKEPCFRDENENFNRIFLPTIYFIIFLTGIVGNGLVILVM 60

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 120

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||  |||||||||||||||||||||| |||||     |
Db        121 VLILAFISLDRYLAIVHATNSQSARKLLAEKAVYVGVWIPALLLTIPDIIFADV-----S 175

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 QGDGRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 235

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
              |||||||||||||||||||||||||||| ||||||:|||:|||||||||||||||||||
Db        236 KTTVILILAFFACWLPYYVGISIDSFILLEVIKQGCEFESVVHKWISITEALAFFHCCLN 295

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 349


RESULT 4
Q7YS92_9EUTH
ID   Q7YS92_9EUTH   PRELIMINARY;   PRT;   352 AA.
AC   Q7YS92;
DT   01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2003, sequence version 1.
DT   21-FEB-2006, entry version 16.
DE   Chemokine receptor CXCR4.
OS   Tupaia chinensis (Chinese tree shrew).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Scandentia; Tupaiidae; Tupaia.
OX   NCBI_TaxID=246437;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Yang M., Ben K.;
RT   "Cloning and sequence analysis of HIV-1 related genes of CD4, CXCR4
RT   and CCR5 from tree shrew.";
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Membrane (By similarity).
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AY177628; AAO47588.2; -; mRNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR   GO; GO:0016494; F:C-X-C chemokine receptor activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR000355; Chmkine_rcpt.
DR   InterPro; IPR001277; CXC_4_rcpt.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00657; CCCHEMOKINER.
DR   PRINTS; PR00645; CXCCHMKINER4.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Membrane; Receptor; Transducer;
KW   Transmembrane.
SQ   SEQUENCE   352 AA;  39719 MW;  606B07A6D46A7D53 CRC64;

  Query Match             90.7%;  Score 1692.5;  DB 2;  Length 352;
  Best Local Similarity   91.2%;  Pred. No. 6.8e-124;
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  Matches  323;  Conservative   15;  Mismatches   11;  Indels    5;  Gaps    1;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              :|||||||||||:|||||||  ||||||:|| ||||||||||| ||||||||||||||||
Db          4 ISIYTSDNYSEELGSGDYDSIKEPCFREENAHFNRIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              |||||||||||||||||||||||||||||||:|:|||| |||||||:|||||||||
Db         64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||||||||||||| ||||||||||||||||:|     |
Db        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 178

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              : :||||||| ||: ||:||||||||||||||||||||||||||||||||||||||||||
Db        179 EAEDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 238

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
              ||||||||||||||||:|||||||||| :|||||:||| ||||||||||||||||||||
Db        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFESTVHKWISITEALAFFHCCLN 298

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              |||||||||||||||||| |:|||||||||||||||||||||||||||||||
Db        299 PILYAFLGAKFKSSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 5
Q8HZU1_CALJA
ID   Q8HZU1_CALJA   PRELIMINARY;   PRT;   352 AA.
AC   Q8HZU1;
DT   01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2003, sequence version 1.
DT   30-MAY-2006, entry version 19.
DE   Chemokine receptor CXCR4.
OS   Callithrix jacchus (Common marmoset).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Platyrrhini; Cebidae; Callitrichinae; Callithrix.
OX   NCBI_TaxID=9483;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22174698; PubMed=12186836; DOI=10.1084/jem.20020468;
RA   LaBonte J.A., Babcock G.J., Patel T., Sodroski J.;
RT   "Blockade of HIV-1 infection of New World monkey cells occurs
RT   primarily at the stage of virus entry.";
RL   J. Exp. Med. 196:431-445(2002).
CC   -!- SUBCELLULAR LOCATION: Membrane (By similarity).
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AF452612; AAN14528.1; -; mRNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR   GO; GO:0016494; F:C-X-C chemokine receptor activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR000355; Chmkine_rcpt.
DR   InterPro; IPR001277; CXC_4_rcpt.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00657; CCCHEMOKINER.
DR   PRINTS; PR00645; CXCCHMKINER4.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Membrane; Receptor; Transducer;
KW   Transmembrane.
SQ   SEQUENCE   352 AA;  39803 MW;  8018A4500FC887C0 CRC64;

  Query Match             90.6%;  Score 1691.5;  DB 2;  Length 352;
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  Best Local Similarity   90.7%;  Pred. No. 8.1e-124;
  Matches  321;  Conservative   18;  Mismatches   10;  Indels    5;  Gaps    1;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              :||||||||:||:|||||||  |||||||:||  ||||||||||  ||||||||||||||||
Db          4 ISIYTSDNYTEEIGSGDYDSIKEPCFREENAHFNRIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              ||||||||||||||||||||||||||||||||:|:||||||||||||:|||||||||
Db         64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGKFLCKAVHVIYTVNLYSS 123

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||||||||||||| ||||||||||||||||||:|     |
Db        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 178

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              : |||||||| ||: ||:||||||||||||||||||||||||||||||||||||||||||
Db        179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 238

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
              ||||||||||||||||:|||||||||| :|:|||:||: ||||||||||||||||||
Db        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIRQGCEFENTVHKWISITEALAFFHCCLN 298

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              ||||||||||||:|||||  |:|||||||||||||||||||||||||||||||
Db        299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 6
Q8HZU0_SAISC
ID   Q8HZU0_SAISC   PRELIMINARY;   PRT;   352 AA.
AC   Q8HZU0;
DT   01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT   01-MAR-2003, sequence version 1.
DT   30-MAY-2006, entry version 19.
DE   Chemokine receptor CXCR4.
OS   Saimiri sciureus (Common squirrel monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Platyrrhini; Cebidae; Saimiriinae; Saimiri.
OX   NCBI_TaxID=9521;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22174698; PubMed=12186836; DOI=10.1084/jem.20020468;
RA   LaBonte J.A., Babcock G.J., Patel T., Sodroski J.;
RT   "Blockade of HIV-1 infection of New World monkey cells occurs
RT   primarily at the stage of virus entry.";
RL   J. Exp. Med. 196:431-445(2002).
CC   -!- SUBCELLULAR LOCATION: Membrane (By similarity).
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AF452613; AAN14529.1; -; mRNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR   GO; GO:0016494; F:C-X-C chemokine receptor activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR000355; Chmkine_rcpt.
DR   InterPro; IPR001277; CXC_4_rcpt.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00657; CCCHEMOKINER.
DR   PRINTS; PR00645; CXCCHMKINER4.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Membrane; Receptor; Transducer;
KW   Transmembrane.
SQ   SEQUENCE   352 AA;  39821 MW;  BF1A21FB0C8D4487 CRC64;
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  Query Match             90.5%;  Score 1689.5;  DB 2;  Length 352;
  Best Local Similarity   90.7%;  Pred. No. 1.2e-123;
  Matches  321;  Conservative   18;  Mismatches   10;  Indels    5;  Gaps    1;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              :|||||||:||:||||||| |||||:|| |||||||||| ||||||||||||||||
Db          4 ISIYTSDNYTEEMGSGDYDSIKEPCFREENAHFNRIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              ||||||||||||||||||||||||||||||:|:||||||||||:|||||||||
Db         64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGKFLCKAVHVIYTVNLYSS 123

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||||||||||| ||||||||||||||||||:|     |
Db        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 178

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              : |||||||| ||: ||:|||||||||||||||||||||||||||||||||||||||||
Db        179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 238

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
              ||||||||||||||||||:|||||||||| :|:|||:||: ||||||||||||||||||
Db        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIRQGCEFENTVHKWISITEALAFFHCCLN 298

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              ||||||||||||:|||||| |:|||||||||||||||||||||||||||||||||
Db        299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 7
CXCR4_PAPAN
ID   CXCR4_PAPAN     STANDARD;      PRT;   352 AA.
AC   P56491;
DT   15-JUL-1998, integrated into UniProtKB/Swiss-Prot.
DT   15-JUL-1998, sequence version 1.
DT   18-APR-2006, entry version 33.
DE   C-X-C chemokine receptor type 4 (CXC-R4) (CXCR-4) (SDF-1 receptor)
DE   (Stromal cell-derived factor 1 receptor) (Fusin) (CD184 antigen).
GN   Name=CXCR4;
OS   Papio anubis (Olive baboon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Catarrhini; Cercopithecidae; Cercopithecinae; Papio.
OX   NCBI_TaxID=9555;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=98346785; PubMed=9683255; DOI=10.1016/S0161-5890(98)00016-9;
RA   Benton P.A., Lee D.R., Kennedy R.C.;
RT   "Sequence comparisons of non-human primate HIV-1 coreceptor
RT   homologues.";
RL   Mol. Immunol. 35:95-101(1998).
CC   -!- FUNCTION: Receptor for the C-X-C chemokine CXCL12/SDF-1.
CC       Transduces a signal by increasing the intracellular calcium ions
CC       level (By similarity).
CC   -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
CC   -!- PTM: Sulfated (By similarity).
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AF031089; AAC63831.1; -; mRNA.
DR   InterPro; IPR000355; Chmkine_rcpt.
DR   InterPro; IPR001277; CXC_4_rcpt.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00657; CCCHEMOKINER.
DR   PRINTS; PR00645; CXCCHMKINER4.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Membrane; Receptor;
KW   Sulfation; Transducer; Transmembrane.
FT   CHAIN         1    352       C-X-C chemokine receptor type 4.
FT                                /FTId=PRO_0000069357.
FT   TOPO_DOM      1     39       Extracellular (Potential).
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FT   TRANSMEM     40     63       1 (Potential).
FT   TOPO_DOM     64     79       Cytoplasmic (Potential).
FT   TRANSMEM     80     99       2 (Potential).
FT   TOPO_DOM    100    110       Extracellular (Potential).
FT   TRANSMEM    111    132       3 (Potential).
FT   TOPO_DOM    133    154       Cytoplasmic (Potential).
FT   TRANSMEM    155    175       4 (Potential).
FT   TOPO_DOM    176    200       Extracellular (Potential).
FT   TRANSMEM    201    220       5 (Potential).
FT   TOPO_DOM    221    240       Cytoplasmic (Potential).
FT   TRANSMEM    241    261       6 (Potential).
FT   TOPO_DOM    262    285       Extracellular (Potential).
FT   TRANSMEM    286    305       7 (Potential).
FT   TOPO_DOM    306    352       Cytoplasmic (Potential).
FT   MOD_RES      21     21       Sulfotyrosine (Potential).
FT   CARBOHYD     11     11       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    109    186       By similarity.
SQ   SEQUENCE   352 AA;  39752 MW;  468E542E1851265A CRC64;

  Query Match             90.3%;  Score 1686.5;  DB 1;  Length 352;
  Best Local Similarity   90.7%;  Pred. No. 2e-123;
  Matches  321;  Conservative   16;  Mismatches   12;  Indels    5;  Gaps    1;

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              :||||||||:||:||||||| ||||||:|| |||||||||||| ||||||||||||||||
Db          4 ISIYTSDNYTEEMGSGDYDSIKEPCFREENAHFNRIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              ||||||||||||||||||||||||||||||||||:|:|||| |||||||:|||||||||
Db         64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||||||||||||| |||||||||||||||||| |     |
Db        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFASV-----S 178

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              : |||||||| ||: ||:||||||||||||||||||||||||||||||||||||||||||
Db        179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 238

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
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Db        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 298

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
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Db        299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 8
CXCR4_MACFA
ID   CXCR4_MACFA    STANDARD;      PRT;   352 AA.
AC   Q28474;
DT   15-JUL-1998, integrated into UniProtKB/Swiss-Prot.
DT   01-NOV-1996, sequence version 1.
DT   18-APR-2006, entry version 35.
DE   C-X-C chemokine receptor type 4 (CXC-R4) (CXCR-4) (SDF-1 receptor)
DE   (Stromal cell-derived factor 1 receptor) (Fusin) (LESTR) (CD184
DE   antigen).
GN   Name=CXCR4;
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RA   Tatsumi M., Takahashi H.;
RT   "Monkey CD4 and fusin are not species barrier for HIV-1 replication.";
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor for the C-X-C chemokine CXCL12/SDF-1.
CC       Transduces a signal by increasing the intracellular calcium ions
CC       level (By similarity).
CC   -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
CC   -!- PTM: Sulfated (By similarity).
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC   ---------------------------------------------------------------------
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CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ----------------------------------------------------------------------
DR   EMBL; D86579; BAA13126.1; -; mRNA.
DR   PIR; G00048; G00048.
DR   InterPro; IPR000355; Chmkine_rcpt.
DR   InterPro; IPR001277; CXC_4_rcpt.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00657; CCCHEMOKINER.
DR   PRINTS; PR00645; CXCCHMKINER4.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Membrane; Receptor;
KW   Sulfation; Transducer; Transmembrane.
FT   CHAIN         1    352       C-X-C chemokine receptor type 4.
FT                                /FTId=PRO_0000069353.
FT   TOPO_DOM      1     39       Extracellular (Potential).
FT   TRANSMEM     40     63       1 (Potential).
FT   TOPO_DOM     64     79       Cytoplasmic (Potential).
FT   TRANSMEM     80     99       2 (Potential).
FT   TOPO_DOM    100    110       Extracellular (Potential).
FT   TRANSMEM    111    132       3 (Potential).
FT   TOPO_DOM    133    154       Cytoplasmic (Potential).
FT   TRANSMEM    155    175       4 (Potential).
FT   TOPO_DOM    176    200       Extracellular (Potential).
FT   TRANSMEM    201    220       5 (Potential).
FT   TOPO_DOM    221    240       Cytoplasmic (Potential).
FT   TRANSMEM    241    261       6 (Potential).
FT   TOPO_DOM    262    285       Extracellular (Potential).
FT   TRANSMEM    286    305       7 (Potential).
FT   TOPO_DOM    306    352       Cytoplasmic (Potential).
FT   MOD_RES      21     21       Sulfotyrosine (Potential).
FT   CARBOHYD     11     11       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    109    186       By similarity.
SQ   SEQUENCE   352 AA;  39753 MW;  432DA6C11859EF8A CRC64;

  Query Match             90.0%;  Score 1679.5;  DB 1;  Length 352;
  Best Local Similarity   90.1%;  Pred. No. 7.1e-123;
  Matches  319;  Conservative   17;  Mismatches   13;  Indels    5;  Gaps    1;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              :|||||||:||:||||||| ||||||:|| |||||||||||| ||||||||||||||||
Db          4 ISIYTSDNYTEEMGSGDYDSIKEPCFREENAHFNRIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              |||||||||||||||||||||:|||||||||||:|:|||| ||||||:|||||||||
Db         64 GYQKKLRSMTDKYRLHLSVADLLYVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||||||||||||| |||||||||||||||||||| |     |
Db        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFASV-----S 178

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              : |||||||| ||: ||:|||||||||||||||||||||||||||||||||||||||||
Db        179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 238

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
              ||||||||||||||||:|||||||||| :|||||:||: |||||||||| |||||||
Db        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALGFFHCCLN 298

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              |||||||||||:|||||| |:|||||||||||||||||||||||||||||||
Db        299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 9
O77488_CERAE
ID   O77488_CERAE   PRELIMINARY;   PRT;   352 AA.
AC   O77488;
DT   01-NOV-1998, integrated into UniProtKB/TrEMBL.
DT   01-NOV-1998, sequence version 1.
DT   30-MAY-2006, entry version 31.
DE   CXCR4 receptor.
OS   Cercopithecus aethiops (Green monkey) (Grivet).
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Catarrhini; Cercopithecidae; Cercopithecinae; Cercopithecus.
OX   NCBI_TaxID=9534;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Murayama Y., Matsunaga S., Inoue-Murayama M.;
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Membrane (By similarity).
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB015943; BAA31327.1; -; mRNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR   GO; GO:0016494; F:C-X-C chemokine receptor activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR000355; Chmkine_rcpt.
DR   InterPro; IPR001277; CXC_4_rcpt.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00657; CCCHEMOKINER.
DR   PRINTS; PR00645; CXCCHMKINER4.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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start | next page

SCORE Search Results Details f

This page gives you Search Results detail for the Application 10785230 and Search Result 2007020
start

GenCore version 6.2

OM protein - protein search, using sw model

Run on: February 6, 2007, 14:15:46 ; Search time 26 Seconds
(without alignments)
1315.579 Million cell updates/sec

Title: US-10-785-230-3
Perfect score: 1867
Sequence: 1 MEPISVSIYTSDNYSEEVGS.....KRGGHSSVSTESESSSFHSS 359

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1679.5	90.0	352	2	G00048	fusin (LESTRA) - c
2	1678.5	89.9	352	2	A45747	neuropeptide Y/pep
3	1631	87.4	353	2	S28787	neuropeptide Y/pep
4	585.5	31.4	367	2	JE0349	interferon-inducib
5	570.5	30.6	360	2	A57160	chemokine (C-C) re
6	551.5	29.5	355	2	JQ1231	interleukin-8 rece
7	550.5	29.5	378	2	A55735	G protein-coupled
8	547.5	29.3	356	2	S42096	interleukin-8 rece
9	544.5	29.2	358	2	A53752	interleukin-8 rece
10	544.5	29.2	360	2	A53611	interleukin-8 rece
11	537.5	28.8	378	2	B55735	lymphocyte-specifi
12	535	28.7	369	2	JC5068	G protein-coupled
13	533	28.5	355	2	JC4304	orphan G protein-c
14	530	28.4	360	2	JC4587	chemokine (C-C) re
15	526.5	28.2	327	2	S56162	MDCR15 protein - h
16	523.5	28.0	359	2	A48921	interleukin-8 rece
17	522.5	28.0	350	2	A39445	interleukin-8 rece
18	522.5	28.0	372	2	S26667	G protein-coupled
19	518.5	27.8	378	2	A45680	G protein-coupled

20	517.5	27.7	374	2	S42628	G protein-coupled
21	508.5	27.2	374	2	S32785	G protein-coupled
22	507	27.2	383	2	S55594	G protein-coupled
23	501	26.8	354	2	I58186	probable G protein
24	496	26.6	374	2	I38450	chemokine (C-C) re
25	494	26.5	355	2	JC5067	G protein-coupled
26	484	25.9	350	2	JN0621	G protein-coupled
27	483.5	25.9	352	2	A43113	chemokine (C-C) re
28	479.5	25.7	360	2	JC2443	chemokine (C-C) re
29	476.5	25.5	355	2	G02436	chemokine (C-C) re
30	473.5	25.4	359	2	S15403	angiotensin II rec
31	472.5	25.3	355	2	A45177	chemokine (C-C) re
32	463.5	24.8	359	2	JC1104	angiotensin II rec
33	463.5	24.8	362	2	JN0694	angiotensin II rec
34	460	24.6	362	2	A30341	G protein-coupled
35	459.5	24.6	359	2	S44425	angiotensin II rec
36	459.5	24.6	359	2	JH0621	angiotensin II rec
37	459.5	24.6	359	2	A42656	angiotensin II rec
38	459.5	24.6	359	2	JC2134	angiotensin II rec
39	457.5	24.5	359	2	A48857	angiotensin II rec
40	453.5	24.3	359	2	JQ1516	angiotensin II rec
41	453	24.3	354	2	A23669	interleukin-8 rece
42	448	24.0	362	2	A39714	G protein-coupled
43	447.5	24.0	359	2	I49341	MIP-1 alpha recept
44	445.5	23.9	359	2	I39418	angiotensin II rec
45	442.5	23.7	359	2	JC1194	angiotensin II rec

ALIGNMENTS

RESULT 1
G00048
fusin (LESTRA) - crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
C;Accession: G00048
R;Tatsumi, M.
submitted to GenBank, July 1996
A;Reference number: H00048
A;Accession: G00048
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-352 <TAT>
A;Cross-references: UNIPROT:Q28474; UNIPARC:UPI0000127302; GB:D86579; NID:g1468948; PID:g1468949
C;Superfamily: vertebrate rhodopsin

Query Match 90.0%; Score 1679.5; DB 2; Length 352;
Best Local Similarity 90.1%; Pred. No. 3.4e-139;
Matches 319; Conservative 17; Mismatches 13; Indels 5; Gaps 1;

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Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              :|||||||:||:|||||| ||||||:|| |||||||||| ||||||||||||||||
Db          4 ISIYTSDNYTEEMGSGDYDSIKEPCFREENAHFNRIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              ||||||||||||||||||||||:||||||||||:|:|||| |||||||:||||||||
Db         64 GYQKKLRSMTDKYRLHLSVADLLYVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
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Db        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFASV-----S 178

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              : |||||||| ||: ||:|||||||||||||||||||||||||||||||||||||||||
Db        179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 238

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
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Db        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALGFFHCCLN 298

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
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Db        299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
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RESULT 2
A45747
neuropeptide Y/peptide YY receptor Y3 - human
N;Alternate names: fusin; HM89; leukocyte-derived seven-transmembrane receptor LESTR; receptor D2S201E
C;Species: Homo sapiens (man)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: A45747; A53103; I53006; I59444; I69203; S32761
R;Federsppiel, B.; Melhado, I.G.; Duncan, A.M.V.; Delaney, A.; Schappert, K.; Clark-Lewis, I.; Jirik, F.R.
Genomics 16, 707-712, 1993
A;Title: Molecular cloning of the cDNA and chromosomal localization of the gene for a putative seven-transm
A;Reference number: A45747; MUID:93315164; PMID:8325644
A;Accession: A45747
A;Molecule type: mRNA
A;Residues: 1-352 <FED>
A;Cross-references: UNIPROT:P61073; UNIPARC:UPI000000106C; GB:M99293; NID:g292516; PIDN:AAA16617.1; PID:g29
R;Loetscher, M.; Geiser, T.; O'Reilly, T.; Zwahlen, R.; Baggiolini, M.; Moser, B.
J. Biol. Chem. 269, 232-237, 1994
A;Title: Cloning of a human seven-transmembrane domain receptor, LESTR, that is highly expressed in leukocy
A;Reference number: A53103; MUID:94103215; PMID:8276799
A;Accession: A53103
A;Molecule type: mRNA
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A;Cross-references: UNIPARC:UPI000000106C; EMBL:X71635; NID:g297099; PIDN:CAA50641.1; PID:g297100
R;Herzog, H.; Hort, Y.J.; Shine, J.; Selbie, L.A.
DNA Cell Biol. 12, 465-471, 1993
A;Title: Molecular cloning, characterization, and localization of the human homolog to the reported bovine
A;Reference number: I53006; MUID:93319629; PMID:8329116
A;Accession: I53006
A;Status: preliminary; translated from GB/EMBL/DDBJ
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R;Jazin, E.E.; Yoo, H.; Blomqvist, A.G.; Yee, F.; Weng, G.; Walker, M.W.; Salon, J.; Larhammar, D.; Wahlest
Regul. Pept. 47, 247-258, 1993
A;Title: A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its human homologue, confers neithe
A;Reference number: I59444; MUID:94052833; PMID:8234909
A;Accession: I59444
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-352 <RE2>
A;Cross-references: UNIPARC:UPI000000106C; GB:L01639; NID:g189313; PIDN:AAA16594.1; PID:g189314
R;Nomura, H.; Nielsen, B.W.; Matsushima, K.
Int. Immunol. 5, 1239-1249, 1993
A;Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte chemotactic peptide rec
A;Reference number: I54751; MUID:94092629; PMID:7505609
A;Accession: I69203
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-352 <RES>
A;Cross-references: UNIPARC:UPI000000106C; GB:D10924; NID:g219868; PIDN:BAA01722.1; PID:g219869
C;Genetics:
A;Gene: GDB:NPY3R; NPYY3
A;Cross-references: GDB:230002; OMIM:162643
A;Map position: 2q21-2q21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 89.9%; Score 1678.5; DB 2; Length 352;
Best Local Similarity 90.1%; Pred. No. 4.2e-139;
Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;

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Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              :|||||||:||:|||||||  ||||||:||  :||:|||||||  ||||||||||||||||
Db          4 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              ||||||||||||||||||||||||||||||:|:|||| |||||||:|||||||||
Db         64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||||||||||||| ||||||||||||||||||:|     |
Db        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 178

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              : |||||||| ||: ||:||||||||||||||||||||||||||||||||||||||||||
Db        179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 238
```

```
Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
              ||||||||||||||||||:|||||||||| :|||||:||: ||||||||||||||||||
Db        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 298

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              ||||||||||||:|||||| |:|||||||||||||||||||||||||||||||
Db        299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 3
S28787
neuropeptide Y/peptide YY receptor Y3 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: S28787
R;Rimland, J.; Xin, W.; Sweetnam, P.; Saijoh, K.; Nestler, E.J.; Duman, R.S.
Mol. Pharmacol. 40, 869-875, 1991
A;Title: Sequence and expression of a neuropeptide Y receptor cDNA.
A;Reference number: S28787; MUID:92100053; PMID:1661837
A;Accession: S28787
A;Molecule type: mRNA
A;Residues: 1-353 <RIM>
A;Cross-references: UNIPROT:P25930; UNIPARC:UPI00001272FF; EMBL:M86739
C;Superfamily: vertebrate rhodopsin
C;Keywords: appetite; G protein-coupled receptor; transmembrane protein

  Query Match             87.4%;  Score 1631;  DB 2;  Length 353;
  Best Local Similarity   86.8%;  Pred. No. 5.9e-135;
  Matches  308;  Conservative   26;  Mismatches   15;  Indels    6;  Gaps    2;

Qy          6 VSIYTSDNYSE-EVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILV 64
              : |:||||||:| ::|||||||| |||||||:|| |||||||||:| ||||||||||||||
Db          4 IRIFTSDNYTEDDLGSGDYDSMKEPCFREENAHFNRIFLPTVYSIIFLTGIVGNGLVILV 63

Qy         65 MGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYS 124
              ||||||||||||||||||||||||||:|||||||||:|:|||||||||||||:||||||||
Db         64 MGYQKKLRSMTDKYRLHLSVADLLFVLTLPFWAVDAVANWYFGKFLCKAVHVIYTVNLYS 123

Qy        125 SVLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDI 184
              |||||||||||||||||||||||:||||||||*||||||:||:|||||| |||     ||
Db        124 SVLILAFISLDRYLAIVHATNSQKPRKLLAEKVVYVGVWLPAVLLTIPDLIFA-----DI 178

Qy        185 SQGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKA 244
               : |:|||||| ||  ||:||||||||:|||:|||||||||||||||||||:|||||
Db        179 KEVDERYICDRFYPSDLWLVVFQFQHIVVGLLLPGIVILSCYCIIISKLSHSKGYQKRKA 238

Qy        245 LKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCL 304
              ||||||||| |||||||||:|||||||||| :|:|||:||| ||||||||||||||||
Db        239 LKTTVILILTFFACWLPYYIGISIDSFILLEIIQQGCEFESTVHKWISITEALAFFHCCL 298

Qy        305 NPILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              ||||||||||||:|||||| |:|||||||||||||||||||||||||||||||||
Db        299 NPILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 353


RESULT 4
JE0349
interferon-inducible protein 10 (IP-10) receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004
C;Accession: JE0349
R;Tamaru, M.; Tominaga, Y.; Yatsunami, K.; Narumi, S.
Biochem. Biophys. Res. Commun. 251, 41-48, 1998
A;Title: Cloning of the murine interferon-inducible protein 10 (IP-10) receptor and its specific expression
A;Reference number: JE0349; MUID:99009219; PMID:9790904
A;Accession: JE0349
A;Molecule type: mRNA
A;Residues: 1-367 <TAM>
A;Cross-references: UNIPROT:Q9QWN6; UNIPARC:UPI0000029B69; DDBJ:AB003174; NID:g3798731; PIDN:BAA34045.1; PI
C;Comment: This protein is important for lymphocyte trafficking to lymphoid organs.
C;Superfamily: vertebrate rhodopsin

  Query Match             31.4%;  Score 585.5;  DB 2;  Length 367;
  Best Local Similarity   35.4%;  Pred. No. 1.5e-43;
  Matches  123;  Conservative   69;  Mismatches  130;  Indels   25;  Gaps    7;
```

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Qy         17 EVGSGDYD-SNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVMGYQKKLRSMT 75
              : |  : | |:  || :| :::|:| ||| :| ::|| |::||| |  |:  |:   | |
Db         28 DYGENESDFSDSPPCPQDFSLNFDRTFLPALYSLLFLLGLLGNGAVAAVLLSQRTALSST 87

Qy         76 DKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSSVLILAFISLD 135
              | : |||:|||:| |:||| ||||   | ||  |||    :: :| |:   :|| || |
Db         88 DTFLLHLAVADVLLVLTLPLWAVDAAVQWVFGPGLCKVAGALFNINFYAGAFLLACISFD 147

Qy        136 RYLAIVHATNSQR--PRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDISQGDDRYI- 192
              |||:|||||  |  ||  :|   :   ||  ||  :||||:       :|   |: :
Db        148 RYLSIVHATQIYRRDPRVRVALTCIV--VWGLCLLFALPDFIY-------LSANYDQRLN 198

Qy        193 ---CDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTV 249
                 |   :|  :     :   :: | :|| :|:  ||  |:: |  |:| :: :|:: |
Db        199 ATHCQYNFP-QVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRFRAMRLVV 257

Qy        250 ILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLNPILY 309
              ::: ||  || ||:: : :|  : :||: : |  || |    |:|  : : ||||||:||
Db        258 VVVAAFAVCWTPYHLVVLVDILMDVGVLARNCGRESHVDVAKSVTSGMGYMHCCLNPLLY 317

Qy        310 AFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSF 356
              ||:| ||:          : |          :||     |:    ||:
Db        318 AFVGVKFREQMWMLFTRLGRSD--------QRGPQRQPSSSRRESSW 356


RESULT 5
A57160
chemokine (C-C) receptor 4 - human
N;Alternate names: C-C CKR-4
C;Species: Homo sapiens (man)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: A57160
R;Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; Wells, T.N.C.
J. Biol. Chem. 270, 19495-19500, 1995
A;Title: Molecular cloning and functional expression of a novel CC chemokine receptor cDNA from a human bas
A;Reference number: A57160; MUID:95370289; PMID:7642634
A;Accession: A57160
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-360 <POW>
A;Cross-references: UNIPROT:P51679; UNIPARC:UPI000002DFE9; GB:X85740; NID:g1370103; PIDN:CAA59743.1; PID:g9
A;Note: source clone K5-5
C;Genetics:
A;Gene: GDB:CMKBR4
A;Cross-references: GDB:677463
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F;40-65/Domain: transmembrane #status predicted <TM1>
F;76-97/Domain: transmembrane #status predicted <TM2>
F;112-133/Domain: transmembrane #status predicted <TM3>
F;151-175/Domain: transmembrane #status predicted <TM4>
F;208-226/Domain: transmembrane #status predicted <TM5>
F;243-264/Domain: transmembrane #status predicted <TM6>
F;291-308/Domain: transmembrane #status predicted <TM7>
F;29-276,110-187/Disulfide bonds: #status predicted
F;72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

  Query Match             30.6%;  Score 570.5;  DB 2;  Length 360;
  Best Local Similarity   37.4%;  Pred. No. 3.1e-42;
  Matches  120;  Conservative   63;  Mismatches  125;  Indels   13;  Gaps    6;

Qy          1 MEPISVSIYTSDNYSEEVGSGD--YDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGN 58
              | |  ::  | |   | : |    |:|  :|| ::    |  :||| :| ::|: |::||
Db          1 MNPTDIADTTLD---ESIYSNYYLYESIPKPCTKEGIKAFGELFLPPLYSLVFVFGLLGN 57

Qy         59 GLVILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIY 118
               :|:||:   |:|||||| | |:|:::|||| :||||   |   | ||  ||| :  :|
Db         58 SVVVLVLFKYKRLRSMTDVYLLNLAISDLLFVFSLPFWGYYAADQWVFGLGLCKMISWMY 117

Qy        119 TVNLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFAD 178
               |  || :  :  :|:||||||||||  | | | |       :  |  |:  ::| |:|:
```

```
Db        118 LVGFYSGIFFVMLMSIDRYLAIVHAVFSLRARTLTYGVITSLATWSVAVFASLPGFLFST 177

Qy        179 VSQGDISQGDDRYICDRLYP--DSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHS 236
                  :: :  | |   |    : | |:   :  ::||::|  ::| || :||  | |
Db        178 C----YTERNHTY-CKTKYSLNSTTWKVLSSLEINILGLVIPLGIMLFCYSMIIRTLQHC 232

Qy        237 KGHQKRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEA 296
              |  :| ||:|    ::: |   | || : : ::: : | |: | | ||  :   |  ||
Db        233 KNEKKNKAVKMIFAVVVLFLGFWTPYNIVLFLETLVELEVL-QDCTFERYLDYAIQATET 291

Qy        297 LAFFHCCLNPILYAFLGAKFK 317
              ||| |||||||:| ||| ||:
Db        292 LAFVHCCLNPIIYFFLGEKFR 312


RESULT 6
JQ1231
interleukin-8 receptor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: JQ1231; A46483
R;Beckmann, M.P.; Munger, W.E.; Kozlosky, C.; VandenBos, T.; Price, V.; Lyman, S.; Gerard, N.P.; Gerard, C.
Biochem. Biophys. Res. Commun. 179, 784-789, 1991
A;Title: Molecular characterization of the interleukin-8 receptor.
A;Reference number: JQ1231; MUID:91378994; PMID:1898400
A;Accession: JQ1231
A;Molecule type: DNA
A;Residues: 1-355 <BEC>
A;Cross-references: UNIPROT:P21109; UNIPARC:UPI000012D4ED; GB:M74240; NID:g165438; PIDN:AAA31375.1; PID:g16
R;Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
J. Immunol. 148, 1261-1264, 1992
A;Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor.
A;Reference number: A46483; MUID:92148149; PMID:1737938
A;Accession: A46483
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-355 <LEE>
A;Cross-references: UNIPARC:UPI000012D4ED; GB:M82873; NID:g165440; PIDN:AAA31376.1; PID:g165441
A;Experimental source: neutrophils
A;Note: sequence extracted from NCBI backbone (NCBIN:81526, NCBIP:81530)
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

  Query Match             29.5%;  Score 551.5;  DB 2;  Length 355;
  Best Local Similarity   35.0%;  Pred. No. 1.4e-40;
  Matches  121;  Conservative   72;  Mismatches  142;  Indels   11;  Gaps    6;

Qy         12 DNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVMGYQKKL 71
              | ::   |    : :  ||        |:  :  || ::||  ::|| ||:||: | :
Db         17 DEFANATGMPPVEKDYSPCLVVTQT-LNKYVVVVIYALVFLLSLLGNSLVMLVILYSRSN 75

Qy         72 RSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSSVLILAF 131
              ||:|| | |:|::::||||| :|:| |||     | ||  ||| | ::  || || :|:||
Db         76 RSVTDVYLLNLAMADLLFALTMPIWAVSKEKGWIFGTPLCKVVSLVKEVNFYSGILLLAC 135

Qy        132 ISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDISQGDDRY 191
              ||:|||||||||| :   :: |  | : :|:|  :|:|::| |:|  |     |  :
Db        136 ISVDRYLAIVHATRTLTQKRHLV-KFICLGIWALSLILSLPFFLFRQV----FSPNNSSP 190

Qy        192 IC--DRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTV 249
              :|  |  :  : | :| :      | ||| :|:| ||   :  |  :   || :|::
Db        191 VCYEDLGHNTAKWRMVLRILPHTFGFILPLLVMLFCYGFTLRTLFQAHMGQKHRAMRVIF 250

Qy        250 ILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLNPILY 309
               ::| |  ||||| : :  |: :   ||:: |   : : : :  || | | | |||||:|
Db        251 AVVLIFLLCWLPYNLVLLADTLMRTHVIQETCQRRNDIDRALDATEILGFLHSCLNPIIY 310

Qy        310 AFLGAKFKSSAQHALNSMSRG-SSLKILSKGKRGGHSSVSTESESS 354
              ||:|  |::     |   :||  | : |:: :   ::| ||   |:
Db        311 AFIGQNFRNGFLKML--AARGLISKEFLTRHRVTSYTSSSTNVPSN 354


RESULT 7
A55735
G protein-coupled receptor EBI1 - mouse
C;Species: Mus musculus (house mouse)
```

C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A55735
R;Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
Genomics 23, 643-650, 1994
A;Title: Cloning of human and mouse EBI1, a lymphoid-specific G-protein-coupled receptor encoded on human c
A;Reference number: A55735; MUID:95154835; PMID:7851893
A;Accession: A55735
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-378 <SCH>
A;Cross-references: UNIPROT:P47774; UNIPARC:UPI00000274D1; GB:L31580; NID:g468340; PIDN:AAA74232.1; PID:g46
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor

  Query Match   29.5%; Score 550.5; DB 2; Length 378;
  Best Local Similarity 33.2%; Pred. No. 1.8e-40;
  Matches 117; Conservative   78; Mismatches 150; Indels   7; Gaps   3;

```
Qy         11 SDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVMGYQKK 70
              :|:|  |  : ||   :. ||: :  :|   ||| :| :|   |::|||||||   | |:
Db         29 TDDYIGENTTVDYTLYESVCFKKDVRNFKAWFLPLMYSVICFVGLLGNGLVILTYIYFKR 88

Qy         71 LRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSSVLILA 130
              |::||| | |:|:|||:||:: |||||      | || :||| :  ||| :: :| :|:|
Db         89 LKTMTDTYLLNLAVADILFLLILPFWAYSEAKSWIFGVYLCKGIFGIYKLSFFSGMLLLL 148

Qy        131 FISLDRYLAIVHAT--NSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDISQGD 188
               ||:|||:||| |   :  | | ||  |   ||:|: || |:||: ::: : :   : |:
Db        149 CISIDRYVAIVQAVSRHRHRARVLLISKLSCVGIWMLALFLSIPELLYSGLQK---NSGE 205

Qy        189 DRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTT 248
              |   | :      ::  |   :: | ::| : :  || |||  |  ::  :: ||:|
Db        206 DTLRCSLVSAQVEALITIQVAQMVFGFLVPMLAMSFCYLIIIRTLLQARNFERNKAIKVI 265

Qy        249 VILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLNPIL 308
              : ::: | ·  |||   :   :     :    |:   ::    :| :||   ||:|| | .
Db        266 IAVVVVFIVFQLPYNGVVLAQTVANFNITNSSCETSKQLNIAYDVTYSLASVRCCVNPFL 325

Qy        309 YAFLGAKFKSSAQHALNSMSRGSS--LKILSKGKRGGHSSVSTESESSSFHS 358
              |||:| ||:|        :   |   |:  | :   ::||| |:|:::  |
Db        326 YAFIGVKFRSDLFKLFKDLGCLSQERLRHWSSCRHVRNASVSMEAETTTTFS 377
```

RESULT 8
S42096
interleukin-8 receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-Aug-1999
C;Accession: S42096
R;Gobl, A.E.; Wang, S.; Zhou, Y.; Oeberg, K.
submitted to the EMBL Data Library, February 1994
A;Description: Molecular cloning of the rat IL8 receptor.
A;Reference number: S42096
A;Accession: S42096
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-356 <GOB>
A;Cross-references: UNIPARC:UPI00001778DE; EMBL:X77797
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

  Query Match   29.3%; Score 547.5; DB 2; Length 356;
  Best Local Similarity 34.8%; Pred. No. 3.1e-40;
  Matches 129; Conservative   67; Mismatches 124; Indels   51; Gaps   11;

```
Qy         12 DNYS-EEVGSGDYD----------SNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGN 58
              ||:| |:  ||| |           |:  ||    |:  ||  :  || :: |  :|||
Db          7 DNFSLEDFFSGDIDSYNFSSDPPFTLSDAAPC-PSANLDINRYAVVVIYVLVTLLSLVGN 65

Qy         59 GLVILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIY 118
               ||:||: | :   |:|| | |:|::||| | :|||  ||   :  | || ||||    :
Db         66 SLVMLVILYNRSTCSVTDVYLLNLAIADLFFALTLPVWAASKVNGWIFGSFLCKVFSFLQ 125

Qy        119 TVNLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFAD 178
              .  :  |||||:|| ||:||||||||||::   :: |  | | : :|  :|:|::| ||
Db        126 EITFYSSVLLLACISMDRYLAIVHATSTLIQKRHLV-KFVCITMWFLSLVLSLPIFIL-- 182
```

```
Qy        179 VSQGDISQGDDRYICDRLYPD-----SLWMVVFQFQHIMVGLILPGIVILSCYCIIISKL 233
                :  :       :|   | :     | | || :      | :|| :::| ||   :  |
Db        183 --RTTVKANPSTVVC---YENIGNNTSKWRVVLRILPQTYGFLLPLLIMLFCYGFTLRTL 237

Qy        234 SHSKGHQKRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISI 293
                :   || :|::    ::| |  ||||| : :  |: :   :||: |: :: ::|
Db        238 FKAHMGQKHRAMRVIFAVVLVFLLCWLPYNIVLFTDTLMRTKLIKETCERQNEINK---A 294

Qy        294 TEALAFFHCCLNPILYAFLGAKFKSSAQHALNSMSRGSSLKILSK---------GKRGGH 344
              :| | | | |||||:|||:| ||:    | |        |||::           | |
Db        295 SEILGFLHSCLNPIIYAFIGQKFR----HGL--------LKIMANYGLVSKEFLAKEGRP 342

Qy        345 SSVSTESESSS 355
              | | : | ::|
Db        343 SFVGSSSANTS 353
```

RESULT 9
A53752
interleukin-8 receptor (clone 5B1a) - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: A53752
R;Prado, G.N.; Thomas, K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Folco, E.; Navarro, J.
J. Biol. Chem. 269, 12391-12394, 1994
A;Title: Molecular characterization of a novel rabbit interleukin-8 receptor isotype.
A;Reference number: A53752; MUID:94230294; PMID:8175642
A;Accession: A53752
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-358 <PRA>
A;Cross-references: UNIPROT:P35344; UNIPARC:UPI000012D4F4; GB:L24445; NID:g437661; PIDN:AAA31378.1; PID:g43
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

  Query Match   29.2%; Score 544.5; DB 2; Length 358;
  Best Local Similarity   34.7%; Pred. No. 5.7e-40;
  Matches 128; Conservative   70; Mismatches 132; Indels   39; Gaps   9;

```
Qy          9 YTSDNYSEEVGSGDYDS------------NKEPCFRDENVHFNRIFLPTIYFIIFLTGIV 56
              :| :||| |   ||: :             :  || | |::  |   :   | ::||  ::
Db          4 FTWENYSYEDFFGDFSNYSYSTDLPPTLLDSAPC-RSESLETNSYVVLITYILVFLLSLL 62

Qy         57 GNGLVILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHI 116
              || ||:||: | :   |:|| | |:|::|||||  ||| ||   :  | ||  ||| | :
Db         63 GNSLVMLVILYSRSTCSVTDVYLLNLAIADLLFATTLPIWAASKVHGWTFGTPLCKVVSL 122

Qy        117 IYTVNLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIF 176
              :  || || :|:|| ||:||||||||||| :   :: |  | : : :|  :|:|::|  :|
Db        123 VKEVNFYSGILLLACISVDRYLAIVHATRTMIQKRHLV-KFICLSMWGVSLILSLPILLF 181

Qy        177 ADVSQGDISQGDDRYICDRLYPD-----SLWMVVFQFQHIMVGLILPGIVILSCYCIIIS 231
               :     |   :   :|   | |     : | :| :      | ||| :|:| ||   :
Db        182 RNA----IFPPNSSPVC---YEDMGNSTAKWRMVLRILPQTFGFILPLLVMLFCYVFTLR 234

Qy        232 KLSHSKGHQKRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWI 291
               |  :   || :|::    ::| |  ||||| : :  |: :   ||:: |:  : : : :
Db        235 TLFQAHMGQKHRAMRVIFAVVLIFLLCWLPYNLVLLTDTLMRTHVIQETCERRNDIDRAL 294

Qy        292 SITEALAFFHCCLNPILYAFLGAKF-----KSSAQHALNSMSRGSSLKILSKGKRGGHSS 346
               || | | | |||||:|||:| ||     |  | | |       | : |:|  |   |
Db        295 DATEILGFLHSCLNPIIYAFIGQKFRYGLLKILAAHGL------ISKEFLAKESR--PSF 346

Qy        347 VSTESESSS 355
              |:: | ::|
Db        347 VASSSGNTS 355
```

RESULT 10
A53611
interleukin-8 receptor type B - human
C;Species: Homo sapiens (man)
C;Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: I37898; I38712; A53611; A39446
R;Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.

J. Biol. Chem. 269, 26381-26389, 1994
A;Title: Comparison of the genomic organization and promoter function for human interleukin-8 receptors A a
A;Reference number: I37898; MUID:95014476; PMID:7929358
A;Accession: I37898
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-360 <RES>
A;Cross-references: UNIPROT:P25025; UNIPARC:UPI000004358A; EMBL:U11869; NID:g511801; PIDN:AAB60656.1; PID:g
A;Accession: I38712
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-15 <RE2>
A;Cross-references: UNIPARC:UPI000000053D; EMBL:U11872; NID:g511808; PIDN:AAA64380.1; PID:g511809; EMBL:U11
R;Sprenger, H.; Lloyd, A.R.; Lautens, L.L.; Bonner, T.I.; Kelvin, D.J.
J. Biol. Chem. 269, 11065-11072, 1994
A;Title: Structure, genomic organization, and expression of the human interleukin-8 receptor B gene.
A;Reference number: A53611; MUID:94209273; PMID:7512557
A;Accession: A53611
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 6-360 <SPR>
A;Cross-references: UNIPARC:UPI00000746D6; GB:M99412; GB:L19593
R;Murphy, P.M.; Tiffany, H.L.
Science 253, 1280-1283, 1991
A;Title: Cloning of complementary DNA encoding a functional human interleukin-8 receptor.
A;Reference number: A39446; MUID:91368200; PMID:1891716
A;Accession: A39446
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 6-360 <MUR>
A;Cross-references: UNIPARC:UPI00000746D6; GB:M73969
C;Comment: This receptor, unlike IL8RA, binds several peptides besides interleukin-8, including GRO, NAP-2,
C;Genetics:
A;Gene: GDB:IL8RB; IL8RA
A;Cross-references: GDB:127868; OMIM:146928
A;Map position: 2q35-2q35
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 29.2%; Score 544.5; DB 2; Length 360;
Best Local Similarity 33.8%; Pred. No. 5.8e-40;
Matches 127; Conservative 72; Mismatches 124; Indels 53; Gaps 10;

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Qy         11 SDNY-----SEEVGSGDYDSNKEPCFRD------ENVHFNRIFLPTIYFIIFLTGIVGNG 59
              ||::      |:: :  | |   |   |       |::  |: |:  || ::||  ::||
Db          8 SDSFEDFWKGEDLSNYSYSSTLPPFLLDAAPCEPESLEINKYFVVIIYALVFLLSLLGNS 67

Qy         60 LVILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYT 119
              ||:||: | :  ||:|| | |:|::|||| :||| ||   :  | || |||| | ::
Db         68 LVMLVILYSRVGRSVTDVYLLNLALADLLFALTLPIWAASKVNGWIFGTFLCKVVSLLKE 127

Qy        120 VNLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIF-AD 178
              || || :|:|| ||:|||||||||| :   :: |  | : : :|  :||| :|  :|
Db        128 VNFYSGILLLACISVDRYLAIVHATRTLTQKRYLV-KFICLSIWGLSLLLALPVLLFRRT 186

Qy        179 VSQGDISQGDDRYICDRLYPD-----SLWMVVFQFQHIMVGLILPGIVILSCYCIIISKL 233
              |   ::|           | |     : | :: :      | |:| :::| ||   :  |
Db        187 VYSSNVSPA--------CYEDMGNNTANWRMLLRILPQSFGFIVPLLIMLFCYGFTLRTL 238

Qy        234 SHSKGHQKRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISI 293
             :   || :|::    ::| |  ||||| : :  |: :   ||:: |:  : : : :
Db        239 FKAHMGQKHRAMRVIFAVVLIFLLCWLPYNLVLLADTLMRTQVIQETCERRNHIDRALDA 298

Qy        294 TEALAFFHCCLNPILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTES-- 351
              || |   | ||||::|||:| ||:    | |       ||||:      |  :| :|
Db        299 TEILGILHSCLNPLIYAFIGQKFR----HGL--------LKILAI-----HGLISKDSLP 341

Qy        352 --------ESSSFHSS 359
                      ||| |:|
Db        342 KDSRPSFVGSSSGHTS 357
```

RESULT 11
B55735
lymphocyte-specific.G protein-coupled receptor EBI1 - human
N;Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1

C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: B55735; S52443
R;Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
Genomics 23, 643-650, 1994
A;Title: Cloning of human and mouse EBI1, a lymphoid-specific G-protein-coupled receptor encoded on human c
A;Reference number: A55735; MUID:95154835; PMID:7851893
A;Accession: B55735
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-378 <SCH>
A;Cross-references: UNIPROT:P32248; UNIPARC:UPI0000001C2F; GB:L31581; NID:g468319; PIDN:AAA74231.1; PID:g46
R;Burgstahler, R.; Kempkes, B.; Staeube, K.; Lipp, M.
submitted to the EMBL Data Library, February 1995
A;Description: The expression of the chemokine receptor BLR2/EBI1 is specifically transactivated by Epstein
A;Reference number: S52443
A;Accession: S52443
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 21-378 <BUR>
A;Cross-references: UNIPARC:UPI000014DEAD; EMBL:X84702
C;Genetics:
A;Gene: GDB:CMKBR7; EBI1; BLR2; CCR7
A;Cross-references: GDB:342065; OMIM:600242
A;Map position: 17q12-17q21.2
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor

  Query Match 28.8%; Score 537.5; DB 2; Length 378;
  Best Local Similarity 32.1%; Pred. No. 2.5e-39;
  Matches 113; Conservative 79; Mismatches 153; Indels 7; Gaps 3;

```
Qy          11 SDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVMGYQKK 70
               :|:|  :  : ||   :  | : :  :|   ||| :| ||   |::||||||:|   | |:
Db          29 TDDYIGDNTTVDYTLFESLCSKKDVRNFKAWFLPIMYSIICFVGLLGNGLVVLTYIYFKR 88

Qy          71 LRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSSVLILA 130
               |::||| | |:|:||||:||::|||||| |   | ||   || :  || :: :| :|:|
Db          89 LKTMTDTYLLNLAVADILFLLTLPFWAYSAAKSWVFGVHFCKLIFAIYKMSFFSGMLLLL 148

Qy         131 FISLDRYLAIVHATNS--QRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDISQGD 188
                ||:|||:||| | ::   | | ||  |   ||:|| | :|:||: :::|: :   |  :
Db         149 CISIDRYVAIVQAVSAHRHRARVLLISKLSCVGIWILATVLSIPELLYSDLQR---SSSE 205

Qy         189 DRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTT 248
                  |  :       :  |   :::| ::| : :  || :||  |  ::  :: ||:|
Db         206 QAMRCSLITEHVEAFITIQVAQMVIGFLVPLLAMSFCYLVIIRTLLQARNFERNKAIKVI 265

Qy         249 VILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLNPIL 308
               : ::: |    |||   :   :     :    |:    ::    :| :||   ||:|| |
Db         266 IAVVVVFIVFQLPYNGVVLAQTVANFNITSSTCELSKQLNIAYDVTYSLACVRCCVNPFL 325

Qy         309 YAFLGAKFKSSAQHALNSMS--RGSSLKILSKGKRGGHSSVSTESESSSFHS 358
               |||:| ||::        :       |:  |  :    ||:| |:|:::  |
Db         326 YAFIGVKFRNDLFKLFKDLGCLSQEQLRQWSSCRHIRRSSMSVEAETTTTFS 377
```

RESULT 12
JC5068
G protein-coupled receptor CKR-L3 - human
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
C;Accession: JC5068
R;Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A;Title: Molecular cloning and RNA expression of two new human chemokine receptor-like genes.
A;Reference number: JC5067; MUID:97040707; PMID:8886020
A;Accession: JC5068
A;Molecule type: DNA
A;Residues: 1-369 <ZAB>
A;Cross-references: UNIPARC:UPI0000043586; EMBL:Z79784; NID:g1668737; PIDN:CAB02144.1; PID:g1668738
C;Comment: This protein belongs to the family of alpha chemokine receptors.
C;Genetics:
A;Gene: GDB:CMKBR6; STRL22; GPR29; CCR6; CKR-L3; GPR-CY4
A;Cross-references: GDB:5370639; OMIM:601835
A;Map position: 6q27-6q27

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C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
F;42-68/Domain: transmembrane #status predicted <TM1>
F;79-99/Domain: transmembrane #status predicted <TM2>
F;115-136/Domain: transmembrane #status predicted <TM3>
F;160-180/Domain: transmembrane #status predicted <TM4>
F;212-233/Domain: transmembrane #status predicted <TM5>
F;250-271/Domain: transmembrane #status predicted <TM6>
F;292-315/Domain: transmembrane #status predicted <TM7>

  Query Match             28.7%;  Score 535;  DB 2;  Length 369;
  Best Local Similarity   33.9%;  Pred. No. 4e-39;
  Matches  124;  Conservative   72;  Mismatches  136;  Indels   34;  Gaps    9;

Qy         10 TSDNYSEEVGSGDY--DSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVMGY 67
              :|::|   | :  |  ||    |   |   |:|:|:|  | :| : |::|| ||::   :
Db          9 SSEDYFVSVNTSYYSVDSEMLLCSLQEVRQFSRLFVPIAYSLICVFGLLGNILVVITFAF 68

Qy         68 QKKLRSMTDKYRLHLSVADLLFVITLPFWAVD-AMADWYFGKFLCKAVHIIYTVNLYSSV 126
               || ||||| | |::::||:|||:|||||||  |  .| |    || :  || :|    :
Db         69 YKKARSMTDVYLLNMAIADILFVLTLPFWAVSHATGAWVFSNATCKLLKGIYAINFNCGM 128

Qy        127 LILAFISLDRYLAIVHATNS--QRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDI 184
              |:|  ||:|||:||| || |   | | |   | : : ||  :::::   |:|   :|
Db        129 LLLTCISMDRYIAIVQATKSFRLRSRTLPRSKIICLVVWGLSVIISSSTFVF---NQKYN 185

Qy        185 SQGDDRYICDRLY----PDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQ 240
              :|| |  :|:  |        | ::     :: |  :| : :: ||  |:  |  :: :
Db        186 TQGSD--VCEPKYQTVSEPIRWKLLMLGLELLFGFFIPLMFMIFCYTFIVKTLVQAQNSK 243

Qy        241 KRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFF 300
              : ||::  : ::| | || :|: : : : :   || : : |  | ::    ::|| |||
Db        244 RHKAIRVIIAVVLVFLACQIPHNMVLLVTA-ANLGKMNRSCQSEKLIGYTKTVTEVLAFL 302

Qy        301 HCCLNPILYAFLGAKFKSSAQHALNSMSRGSSLKILS-------KGKRGGHSSVSTESES 353
              ||||||:||||:| ||            |   ||||        | |  | |     ||:
Db        303 HCCLNPVLYAFIGQKF------------RNYFLKILKDLWCVRRKYKSSGFSCAGRYSEN 350

Qy        354 SSFHSS 359
               |  :|
Db        351 ISRQTS 356


RESULT 13
JC4304
orphan G protein-coupled receptor - human
N;Alternate names: V28 protein
C;Species: Homo sapiens (man)
C;Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: JC4304
R;Raport, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
Gene 163, 295-299, 1995
A;Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related to genes for chemokine
A;Reference number: JC4304; MUID:96011651; PMID:7590284
A;Accession: JC4304
A;Molecule type: mRNA
A;Residues: 1-355 <RAP>
A;Cross-references: UNIPROT:P49238; UNIPARC:UPI0000000A0B; GB:U20350; NID:g665580; PIDN:AAA91783.1; PID:g66
A;Experimental source: peripheral blood mononuclear cell
C;Comment: This protein is a cell-surface receptor which recognizes extracellular signals and transduces th
C;Comment: This protein is a key regulator of many immune and homeostatic responses, and interacts between
C;Genetics:
A;Gene: v28
A;Map position: 3pter-p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; lymphokine; transmembrane protein
F;35-57/Domain: transmembrane #status predicted <TM1>
F;66-88/Domain: transmembrane #status predicted <TM2>
F;104-125/Domain: transmembrane #status predicted <TM3>
F;146-165/Domain: transmembrane #status predicted <TM4>
F;197-217/Domain: transmembrane #status predicted <TM5>
F;230-254/Domain: transmembrane #status predicted <TM6>
F;275-296/Domain: transmembrane #status predicted <TM7>

  Query Match             28.5%;  Score 533;  DB 2;  Length 355;
  Best Local Similarity   33.1%;  Pred. No. 5.7e-39;
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  Matches  120;  Conservative   65;  Mismatches  146;  Indels   32;  Gaps    7;

Qy       12 DNYSEEVGSG-DYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVMGYQKK 70
Db        2 DQFPESVTENFEYDDLAEACYIGDIVVFGTVFLSIFYSVIFAIGLVGNLLVVFALTNSKK 61

Qy       71 LRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSSVLILA 130
Db       62 PKSVTDIYLLNLALSDLLFVATLPFWTHYLINEKGLHNAMCKFTTAFFFIGFFGSIFFIT 121

Qy      131 FISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDISQGDDR 190
Db      122 VISIDRYLAIVLAANSMNNRTVQHGVTISLGVWAAAILVAAPQFMFTKQKENE------- 174

Qy      191 YICDRLYPD---SLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 247
Db      175 --CLGDYPEVLQEIWPVLRNVETNFLGFLLPLLIMSYCYFRIIQTLFSCKNHKKAKAIKL 232

Qy      248 TVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLNPI 307
Db      233 ILLVVIVFFLFWTPYNVMIFLETLKLYDFF-PSCDMRKDLRLALSVTETVAFSHCCLNPL 291

Qy      308 LYAFLGAKFKSSAQHALNSMSRGSSLKIL----------SKGKRGGHSSVSTESESSSF 356
Db      292 IYAFAGEKFRRYLYHLY-----GKCLAVLCGRSVHVDFSSSESQRSRHGSVL--SSNFTY 344

Qy      357 HSS 359
Db      345 HTS 347


RESULT 14
JC4587
chemokine (C-C) receptor 4 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: JC4587
R;Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
Biochem. Biophys. Res. Commun. 218, 337-343, 1996
A;Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to murine and human C
A;Reference number: JC4587; MUID:96136324; PMID:8573157
A;Accession: JC4587
A;Molecule type: mRNA
A;Residues: 1-360 <HOO>
A;Cross-references: UNIPROT:P51680; UNIPARC:UPI0000028F3B; EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:
A;Experimental source: thymus
C;Genetics:
A;Gene: cc ckr-4
C;Superfamily: vertebrate rhodopsin
C;Keywords: glycoprotein; phosphoprotein; receptor; thymus
F;2,183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

  Query Match             28.4%;  Score 530;  DB 2;  Length 360;
  Best Local Similarity   36.4%;  Pred. No. 1.1e-38;
  Matches  108;  Conservative   62;  Mismatches  119;  Indels    8;  Gaps    4;

Qy       23 YDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVMGYQKKLRSMTDKYRLHL 82
Db       22 YESMPKPCTKEGIKAFGEVFLPPLYSLVFLLGLFGNSVVVLVLFKYKRLKSMTDVYLLNL 81

Qy       83 SVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSSVLILAFISLDRYLAIVH 142
Db       82 AISDLLFVLSLPFWGYYAADQWVFGLGLCKIVSWMYLVGFYSGIFFIMLMSIDRYLAIVH 141

Qy      143 ATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDISQGDDRYICDRLYP--DS 200
Db      142 AVFSLKARTLTYGVITSLITWSVAVFASLPGLLFSTC----YTEHNHTY-CKTQYSVNST 196

Qy      201 LWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTVILILAFFACWL 260
Db      197 TWKVLSSLEINVLGLLIPLGIMLFWYSMIIRTLQHCKNEKKNRAVRMIFGVVVLFLGFWT 256

Qy      261 PYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLNPILYAFLGAKFK 317
```

```
              || | : ::: : | |: | |  |  :   |  || | | ||||||::| ||| ||:
Db        257 PYNVVLFLETLVELEVL-QDCTLERYLDYAIQATETLGFIHCCLNPVIYFFLGEKFR 312


RESULT 15
S56162
MDCR15 protein - human
C;Species: Homo sapiens (man)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999
C;Accession: S56162
R;Barella, L.; Loetscher, M.; Tobler, A.; Baggiolini, M.; Moser, B.
Biochem. J. 309, 773-779, 1995
A;Title: Sequence variation of a novel heptahelical leucocyte receptor through alternative transcript forma
A;Reference number: S56162; MUID:95366951; PMID:7639692
A;Accession: S56162
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-327 <BAR>
A;Cross-references: UNIPARC:UPI000016AD1F; EMBL:X68829; NID:g840783; PIDN:CAA48723.1; PID:g840784
C;Superfamily: vertebrate rhodopsin

  Query Match             28.2%;  Score 526.5;  DB 2;  Length 327;
  Best Local Similarity   34.6%;  Pred. No. 1.9e-38;
  Matches  111;  Conservative   66;  Mismatches  139;  Indels    5;  Gaps    4;

Qy         38 FNRIFLPTIYFIIFLTGIVGNGLVILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWA 97
              |  :|:|  | :||| |::|| ||:.:::   :: || |: :  ||:|||| |  |||
Db          4 FKAVFVPVAYSLIFLLGVIGNVLVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAV 63

Qy         98 VDAMADWYFGKFLCKAVHIIYTVNLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKA 157
               :    |  | |||| |  :: || | | |:|| |::|||||||||| :: | |:||:
Db         64 AEGSVGWVLGTFLCKTVIALHKVNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHI 123

Qy        158 VYVGVWIPALLLTIPDFIFADVSQGDISQGDDR--YICDRLYPDSLWMVVFQFQHIMVGL 215
                 :|:   || :|: :|| ||||  :    |  :  :       |    :| : : |
Db        124 TCGTIWLVGFLLALPEILFAKVSQGHHNNSLPRCTFSQENQAETHAWF-TSRFLYHVAGF 182

Qy        216 ILPGIVILSCYCIIISKLSHSKGH-QKRKALKTTVILILAFFACWLPYYVGISIDSFILL 274
              :|| :|:  ||  :: :|  ::   |::||::  :::  || || ||:: | :|:   |
Db        183 LLPMLVMGWCYVGVVHRLRQAQRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARL 242

Qy        275 GVIKQGCDFESIVHKWISITEALAFFHCCLNPILYAFLGAKFKSSAQHALNSMSRGSSLK 334
               :   |     :   |:: | |   ||||||:|| | | ||:|     |  :   |
Db        243 KAVDNTCKLNGSLPVAITMCEFLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTSPAS 302

Qy        335 ILSKGKRGGHSSVSTESESSS 355
              :         ||:| |||:::
Db        303 LCQLFPSWRRSSLS-ESENAT 322


Search completed: February  6, 2007, 14:23:55
Job time : 27.256 secs
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start

SCORE Search Results Details for Application 10785230 and Search Result 20070206_074028_us-10-785-230-3.rai.

This page gives you Search Results detail for the Application 10785230 and Search Result 20070206_074028_us-10-785-230-3.rai.

start | next page

Go Back to previous page

GenCore version 6.2

OM protein - protein search, using sw model

Run on: February 6, 2007, 14:23:25 ; Search time 39 Seconds
(without alignments)
808.237 Million cell updates/sec

Title: US-10-785-230-3
Perfect score: 1867
Sequence: 1 MEPISVSIYTSDNYSEEVGS.....KRGGHSSVSTESESSSFHSS 359

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1678.5	89.9	352	1	US-08-202-056-3	Sequence 3, Appli
2	1678.5	89.9	352	1	US-08-076-093A-4	Sequence 4, Appli
3	1678.5	89.9	352	1	US-08-701-265-4	Sequence 4, Appli
4	1678.5	89.9	352	1	US-08-284-586-4	Sequence 4, Appli
5	1678.5	89.9	352	1	US-08-805-478-4	Sequence 4, Appli
6	1678.5	89.9	352	1	US-08-802-627A-4	Sequence 4, Appli
7	1678.5	89.9	352	1	US-08-801-238-4	Sequence 4, Appli
8	1678.5	89.9	352	1	US-08-801-228-4	Sequence 4, Appli
9	1678.5	89.9	352	2	US-09-104-296-4	Sequence 4, Appli

10	1678.5	89.9	352	2	US-09-517-605-4	Sequence 4, Appli
11	1678.5	89.9	352	2	US-09-647-501-2	Sequence 2, Appli
12	1672.5	89.6	352	2	US-09-826-509-485	Sequence 485, App
13	1641.5	87.9	352	1	US-08-450-393A-6	Sequence 6, Appli
14	1641.5	87.9	352	2	US-08-446-669-6	Sequence 6, Appli
15	1641.5	87.9	352	2	US-09-625-573-6	Sequence 6, Appli
16	1641.5	87.9	352	5	PCT-US95-00476-6	Sequence 6, Appli
17	1621.5	86.9	337	1	US-08-153-848-46	Sequence 46, Appl
18	1621.5	86.9	337	2	US-09-299-843A-46	Sequence 46, Appl
19	1621.5	86.9	337	2	US-09-088-337B-46	Sequence 46, Appl
20	1621.5	86.9	337	5	PCT-US93-11153-46	Sequence 46, Appl
21	584	31.3	368	2	US-08-709-838-2	Sequence 2, Appli
22	584	31.3	368	2	US-08-829-839-2	Sequence 2, Appli
23	584	31.3	368	2	US-09-170-496D-20	Sequence 20, Appl
24	584	31.3	368	2	US-09-624-594-2	Sequence 2, Appli
25	584	31.3	368	2	US-09-607-156-2	Sequence 2, Appli
26	584	31.3	368	3	US-09-633-541-2	Sequence 2, Appli
27	580	31.1	368	2	US-09-170-496D-174	Sequence 174, App
28	570.5	30.6	360	2	US-08-875-573-20	Sequence 20, Appl
29	570.5	30.6	360	2	US-09-232-878-2	Sequence 2, Appli
30	570.5	30.6	360	2	US-09-045-583-55	Sequence 55, Appl
31	570.5	30.6	360	2	US-09-534-185-55	Sequence 55, Appl
32	570.5	30.6	360	2	US-08-939-107-34	Sequence 34, Appl
33	570.5	30.6	360	2	US-10-039-659A-16	Sequence 16, Appl
34	570.5	30.6	360	2	US-09-067-447B-34	Sequence 34, Appl
35	570.5	30.6	360	2	US-09-837-446-2	Sequence 2, Appli
36	570.5	30.6	360	2	US-09-764-413-20	Sequence 20, Appl
37	570.5	30.6	360	2	US-09-796-744-17	Sequence 17, Appl
38	570.5	30.6	360	3	US-09-509-165A-34	Sequence 34, Appl
39	565.5	30.3	123	2	US-08-513-974B-330	Sequence 330, App
40	558.5	29.9	360	2	US-08-833-752-10	Sequence 10, Appl
41	558.5	29.9	360	2	US-09-938-719-10	Sequence 10, Appl
42	558.5	29.9	360	2	US-09-939-226B-10	Sequence 10, Appl
43	558.5	29.9	360	2	US-09-938-703B-10	Sequence 10, Appl
44	550.5	29.5	378	2	US-09-299-843A-66	Sequence 66, Appl
45	550.5	29.5	378	2	US-09-088-337B-66	Sequence 66, Appl

ALIGNMENTS

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RESULT 1
US-08-202-056-3
; Sequence 3, Application US/08202056
; Patent No. 5440021
;  GENERAL INFORMATION:
;    APPLICANT:  Chuntharapai, Anan
;    APPLICANT:  Hebert, Caroline
;    APPLICANT:  Kim, Kyung Jin
;    APPLICANT:  Lee, James
;    TITLE OF INVENTION:  Antibodies to Human IL-8 Type B Receptor
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/202,056
;      FILING DATE:  25-FEB-1994
;      CLASSIFICATION:  436
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/677211
;      FILING DATE:  29-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  706P3
;    TELECOMMUNICATION INFORMATION:
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;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  352 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-202-056-3

  Query Match             89.9%;  Score 1678.5;  DB 1;  Length 352;
  Best Local Similarity   90.1%;  Pred. No. 1.1e-132;
  Matches  319;  Conservative   19;  Mismatches   11;  Indels    5;  Gaps    1;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
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Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
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Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
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Db        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 178

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
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Db        179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 238

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Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
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Db        299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 2
US-08-076-093A-4
; Sequence 4, Application US/08076093A
; Patent No. 5543503
;  GENERAL INFORMATION:
;    APPLICANT:  Chuntharapai, Anan
;    APPLICANT:  Lee, James
;    APPLICANT:  Hebert, Caroline
;    APPLICANT:  Jin Kim, K.
;    TITLE OF INVENTION:  Antibodies to Human PF4A Receptors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/076,093A
;      FILING DATE:  11-Jun-1993
;      CLASSIFICATION:  530.
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/810782
;      FILING DATE:  19-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/677211
;      FILING DATE:  29-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  706P2
```

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;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  352 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-076-093A-4

  Query Match             89.9%;  Score 1678.5;  DB 1;  Length 352;
  Best Local Similarity   90.1%;  Pred. No. 1.1e-132;
  Matches  319;  Conservative   19;  Mismatches   11;  Indels    5;  Gaps    1;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
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Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
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Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
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RESULT 3
US-08-701-265-4
; Sequence 4, Application US/08701265
; Patent No. 5776457
;  GENERAL INFORMATION:
;    APPLICANT:  Chuntharapai, Anan
;    APPLICANT:  Lee, James
;    APPLICANT:  Hebert, Caroline
;    APPLICANT:  Jin Kim, K.
;    TITLE OF INVENTION:  Antibodies to Human PF4A Receptors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/701,265
;      FILING DATE:  22-AUG-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/076093
;      FILING DATE:  11-Jun-1993
;      APPLICATION NUMBER:  07/810782
;      FILING DATE:  19-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/677211
;      FILING DATE:  29-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
```

```
;     NAME:  Love, Richard B
;       REGISTRATION NUMBER:  34,659
;       REFERENCE/DOCKET NUMBER:  706P2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415/225-5530
;       TELEFAX:  415/952-9881
;       TELEX:  910/371-7168
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  352 amino acids
;       TYPE:  Amino Acid
;       TOPOLOGY:  Linear
US-08-701-265-4

  Query Match             89.9%;  Score 1678.5;  DB 1;  Length 352;
  Best Local Similarity   90.1%;  Pred. No. 1.1e-132;
  Matches  319;  Conservative   19;  Mismatches   11;  Indels    5;  Gaps    1;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
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Db          4 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

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Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
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RESULT 4
US-08-284-586-4
; Sequence 4, Application US/08284586
; Patent No. 5840856
;  GENERAL INFORMATION:
;     APPLICANT:  Chuntharapai, Anan
;     APPLICANT:  Lee, James
;     APPLICANT:  Hebert, Caroline
;     APPLICANT:  Jin Kim, K.
;     TITLE OF INVENTION:  Antibodies to Human PF4A Receptors
;     NUMBER OF SEQUENCES:  6
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Genentech, Inc.
;       STREET:  460 Point San Bruno Blvd
;       CITY:  South San Francisco
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94080
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  WinPatin (Genentech)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/284,586
;       FILING DATE:
;       CLASSIFICATION:  424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/076,093A
;       FILING DATE:  11-Jun-1993
;       APPLICATION NUMBER:  07/810782
;       FILING DATE:  19-DEC-1991
;     PRIOR APPLICATION DATA:
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;      APPLICATION NUMBER:  07/677211
;      FILING DATE:  29-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  706P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  352 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-284-586-4

  Query Match             89.9%;  Score 1678.5;  DB 1;  Length 352;
  Best Local Similarity   90.1%;  Pred. No. 1.1e-132;
  Matches  319;  Conservative   19;  Mismatches   11;  Indels    5;  Gaps    1;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              :|||||||:||:|||||||  |||||:|| :||:|||||||  ||||||||||||||||
Db          4 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              |||||||||||||||||||||||||||||||:|:|||| |||||||:|||||||||
Db         64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
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Db        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 178

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              : |||||||| ||: ||:||||||||||||||||||||||||||||||||||||||||||
Db        179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 238

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
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Db        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 298

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
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Db        299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 5
US-08-805-478-4
; Sequence 4, Application US/08805478
; Patent No. 5874543
;  GENERAL INFORMATION:
;    APPLICANT:  Chuntharapai, Anan
;    APPLICANT:  Lee, James
;    APPLICANT:  Hebert, Caroline
;    APPLICANT:  Jin Kim, K.
;    TITLE OF INVENTION:  ANTIBODIES TO PF4A RECEPTOR
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/805,478
;      FILING DATE:  25-Feb-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/284586
;      FILING DATE:  10-AUG-1994
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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/076093
;      FILING DATE:  11-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/810782
;      FILING DATE:  19-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P0706P2P1C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  352 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-805-478-4

  Query Match             89.9%;  Score 1678.5;  DB 1;  Length 352;
  Best Local Similarity   90.1%;  Pred. No. 1.1e-132;
  Matches  319;  Conservative   19;  Mismatches   11;  Indels    5;  Gaps    1;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              :||||||||:||:||||||| ||||||:|| :||:|||||||| ||||||||||||||||
Db          4 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              ||||||||||||||||||||||||||||||||:|:|||| |||||||:|||||||||
Db         64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||||||||||||| ||||||||||||||||||:|     |
Db        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 178

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              : |||||||| ||: ||:||||||||||||||||||||||||||||||||||||||||||
Db        179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 238

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
              ||||||||||||||||:|||||||||| :|||||:||: ||||||||||||||||||
Db        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 298

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              ||||||||||||:|||||| |:||||||||||||||||||||||||||||||||
Db        299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 6
US-08-802-627A-4
; Sequence 4, Application US/08802627A
; Patent No. 5892017
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, James
;    APPLICANT:  Wood, William I.
;    TITLE OF INVENTION:  NUCLEIC ACID ENCODING PF4A RECEPTOR
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/802,627A
;      FILING DATE:  19-Feb-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
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;      APPLICATION NUMBER:  08/284586
;      FILING DATE:  10-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/076093
;      FILING DATE:  11-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/810782
;      FILING DATE:  19-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P0706P2P1D2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  352 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-802-627A-4

  Query Match             89.9%;  Score 1678.5;  DB 1;  Length 352;
  Best Local Similarity   90.1%;  Pred. No. 1.1e-132;
  Matches  319;  Conservative   19;  Mismatches   11;  Indels    5;  Gaps    1;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              :||||||||:||:||||||| |||||:|| :||:||||||| ||||||||||||||||
Db          4 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              ||||||||||||||||||||||||||||||||:|:|||| |||||||:|||||||||
Db         64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||||||||||||| ||||||||||||||||||:|     |
Db        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 178

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              : |||||||| ||: ||:|||||||||||||||||||||||||||||||||||||||||
Db        179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 238

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
              ||||||||||||||||||:|||||||||| :|||||:||: ||||||||||||||||||
Db        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 298

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              |||||||||||:|||||| |:|||||||||||||||||||||||||||||||||
Db        299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 7
US-08-801-238-4
; Sequence 4, Application US/08801238
; Patent No. 5919896
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, James
;    APPLICANT:  Wood, William I.
;    TITLE OF INVENTION:  PF4A RECEPTOR
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/801,238
;      FILING DATE:  19-Feb-1997
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;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/284586
;      FILING DATE:  10-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/076093
;      FILING DATE:  11-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/810782
;      FILING DATE:  19-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P0706P2P1D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  352 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-801-238-4

  Query Match             89.9%;  Score 1678.5;  DB 1;  Length 352;
  Best Local Similarity   90.1%;  Pred. No. 1.1e-132;
  Matches  319;  Conservative   19;  Mismatches   11;  Indels    5;  Gaps    1;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              :||||||||:||:||||||| ||||||:|| :||:||||||| ||||||||||||||||
Db          4 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              ||||||||||||||||||||||||||||||||:|:|||| |||||||:||||||||
Db         64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||||||||||||| ||||||||||||||||||:|     |
Db        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 178

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
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Db        179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 238

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
              ||||||||||||||||:|||||||||| :||||:||: ||||||||||||||||||
Db        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 298

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              ||||||||||||:|||||| |:|||||||||||||||||||||||||||||||
Db        299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 8
US-08-801-228-4
; Sequence 4, Application US/08801228
; Patent No. 5922541
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, James
;    APPLICANT:  Wood, William I.
;    TITLE OF INVENTION:  METHODS FOR DETECTION AND AMPLIFICATION OF
;    TITLE OF INVENTION:  PF4A RECEPTOR NUCLEIC ACID
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/801,228
;      FILING DATE:  19-Feb-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/284586
;      FILING DATE:  10-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/076093
;      FILING DATE:  11-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/810782
;      FILING DATE:  19-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P0706P2P1D3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  352 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-801-228-4

  Query Match             89.9%;  Score 1678.5;  DB 1;  Length 352;
  Best Local Similarity   90.1%;  Pred. No. 1.1e-132;
  Matches  319;  Conservative   19;  Mismatches   11;  Indels    5;  Gaps    1;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              :||||||||:||:||||||| ||||||:|| :||:||||||| ||||||||||||||||
Db          4 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              ||||||||||||||||||||||||||||||||:|:|||| |||||||:|||||||||
Db         64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              ||||||||||||||||||||||||||| |||||||||||||||||:|     |
Db        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 178

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              : |||||||| ||: ||:||||||||||||||||||||||||||||||||||||||||
Db        179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 238

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
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Db        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 298

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
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Db        299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 9
US-09-104-296-4
; Sequence 4, Application US/09104296
; Patent No. 6087475
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, James
;    APPLICANT:  Wood, WIlliam I.
;    TITLE OF INVENTION:  PF4A Receptors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
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;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  WinPatin (Genentech)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/104,296
;       FILING DATE:  24-June-1998
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/701265
;       FILING DATE:  22-AUG-1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/664228
;       FILING DATE:  06-JUN-1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/076093
;       FILING DATE:  11-JUN-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/810782
;       FILING DATE:  19-DEC-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Love, Richard B.
;       REGISTRATION NUMBER:  34,659
;       REFERENCE/DOCKET NUMBER:  P0706P2C2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415/225-5530
;       TELEFAX:  415/952-9881
;       TELEX:  910/371-7168
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  352 amino acids
;       TYPE:  Amino Acid
;       TOPOLOGY:  Linear
US-09-104-296-4

  Query Match             89.9%;  Score 1678.5;  DB 2;  Length 352;
  Best Local Similarity   90.1%;  Pred. No. 1.1e-132;
  Matches  319;  Conservative   19;  Mismatches   11;  Indels    5;  Gaps    1;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              :||||||||:||:||||||| ||||||:|| :||:||||||| ||||||||||||||||
Db          4 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              ||||||||||||||||||||||||||||||||:|:|||| |||||||:|||||||||
Db         64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
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Db        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 178

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              : |||||||| ||: ||:||||||||||||||||||||||||||||||||||||||||||
Db        179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 238

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
              ||||||||||||||||:|||||||||| :|||||:||: ||||||||||||||||||
Db        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 298

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
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Db        299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 10
US-09-517-605-4
; Sequence 4, Application US/09517605
; Patent No. 6391567
; GENERAL INFORMATION:
;  APPLICANT: Littman, Dan R.
;  APPLICANT: Kwon, Douglas S.
;  APPLICANT: van Kooyk, Yvette
;  APPLICANT: Geijtenbeck, Tneo
;  TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
;  TITLE OF INVENTION: CELLS
;  FILE REFERENCE: 1049-1-017
;  CURRENT APPLICATION NUMBER: US/09/517,605
;  CURRENT FILING DATE: 2000-03-02
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;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-517-605-4

  Query Match             89.9%;  Score 1678.5;  DB 2;  Length 352;
  Best Local Similarity   90.1%;  Pred. No. 1.1e-132;
  Matches  319;  Conservative   19;  Mismatches   11;  Indels    5;  Gaps    1;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              :||||||||:||:|||||||  ||||||:||  :||:|||||||  ||||||||||||||||
Db          4 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              ||||||||||||||||||||||||||||||||||:|:||||  |||||||:|||||||||
Db         64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||||||||||||| ||||||||||||||||||:|     |
Db        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 178

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              : |||||||| ||: ||:||||||||||||||||||||||||||||||||||||||||||
Db        179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 238

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
              ||||||||||||||||:||||||||||  :|||||:||: ||||||||||||||||||
Db        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 298

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              ||||||||||||:|||||| |:|||||||||||||||||||||||||||||||||
Db        299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 11
US-09-647-501-2
; Sequence 2, Application US/09647501
; Patent No. 6863887
; GENERAL INFORMATION:
;  APPLICANT: No. 6863887thwest Biotherapeutics, Inc.
;  APPLICANT:  Murphy, Gerald P.
;  APPLICANT:  Boynton, Alton L.
;  APPLICANT:  Sehgal, Anil
;  TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED ON THE
;  TITLE OF INVENTION:  ROLE OF THE CXCR-4 GENE IN TUMORIGENESIS
;  FILE REFERENCE: 20093-000600PC
;  CURRENT APPLICATION NUMBER: US/09/647,501
;  CURRENT FILING DATE:  2000-09-24
;  PRIOR APPLICATION NUMBER: 60/079,916
;  PRIOR FILING DATE: 1998-03-30
;  PRIOR APPLICATION NUMBER: 60/104,656
;  PRIOR FILING DATE: 1998-10-16
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-647-501-2

  Query Match             89.9%;  Score 1678.5;  DB 2;  Length 352;
  Best Local Similarity   90.1%;  Pred. No. 1.1e-132;
  Matches  319;  Conservative   19;  Mismatches   11;  Indels    5;  Gaps    1;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              :||||||||:||:|||||||  ||||||:||  :||:|||||||  ||||||||||||||||
Db          4 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
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Db         64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
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Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              : |||||||| ||: ||:||||||||||||||||||||||||||||||||||||||||||
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Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
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Db        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 298

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
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Db        299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 12
US-09-826-509-485
; Sequence 485, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
;  APPLICANT: Lehmann-Bruinsma, Karin
;  APPLICANT:  Liaw, Chen W.
;  APPLICANT:  Lin, I-Lin
;  TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
;  TITLE OF INVENTION:  Protein-Coupled Receptors
;  FILE REFERENCE: AREN-207
;  CURRENT APPLICATION NUMBER: US/09/826,509
;  CURRENT FILING DATE:  2001-04-05
;  PRIOR APPLICATION NUMBER: 60/195,747
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: 09/170,496
;  PRIOR FILING DATE: 1998-10-13
;  NUMBER OF SEQ ID NOS: 589
;  SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 485
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-826-509-485

  Query Match             89.6%;  Score 1672.5;  DB 2;  Length 352;
  Best Local Similarity   89.8%;  Pred. No. 3.6e-132;
  Matches  318;  Conservative   19;  Mismatches   12;  Indels    5;  Gaps    1;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              :||||||||:||:||||||| |||||:|| :|||:||||||| ||||||||||||||||
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Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              ||||||||||||||||||||||||||||||:|:|||| |||||||:||||||||
Db         64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||||||||||||| ||||||||||||||||||:|     |
Db        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 178

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
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Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
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Db        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 298

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              ||||||||||||:|||||| |:|||||||||||||||||||||||||||||||
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RESULT 13
US-08-450-393A-6
; Sequence 6, Application US/08450393A
; Patent No. 5707815
;  GENERAL INFORMATION:
;    APPLICANT:  Charo, Israel
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; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816CooleyPA
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid

start | next page

SCORE Search Results Details for Application 10785230 and Search Result 20070206_074033_us-10-785-230-3.rapbm.

This page gives you Search Results detail for the Application 10785230 and Search Result 20070206_074033_us-10-785-230-3.rapbm.

start

Go Back to previous page

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                    GenCore version 6.2
                Copyright (c) 1993 - 2007  Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:         February  6, 2007, 14:24:16 ; Search time 137 Seconds
                                        (without alignments)
                                        1215.298 Million cell updates/sec

Title:          US-10-785-230-3
Perfect score:  1867
Sequence:       1 MEPISVSIYTSDNYSEEVGS.........KRGGHSSVSTESESSSFHSS 359

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters:      2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        Published_Applications_AA_Main:*
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                2:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
                3:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
                4:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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                6:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                    SUMMARIES

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Result           Query
   No.   Score   Match  Length DB  ID                          Description
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     1    1867   100.0     359  4  US-10-785-230-3             Sequence 3, Appli
     2    1822    97.6     355  5  US-10-330-773-918           Sequence 918, App
     3  1744.5    93.4     349  6  US-11-028-922A-2            Sequence 2, Appli
     4  1678.5    89.9     352  3  US-09-953-692-2             Sequence 2, Appli
     5  1678.5    89.9     352  3  US-09-953-717-2             Sequence 2, Appli
     6  1678.5    89.9     352  3  US-09-104-063-4             Sequence 4, Appli
     7  1678.5    89.9     352  3  US-09-813-651B-85           Sequence 85, Appl
     8  1678.5    89.9     352  4  US-10-151-274-4             Sequence 4, Appli
     9  1678.5    89.9     352  4  US-10-225-567A-76           Sequence 76, Appl
    10  1678.5    89.9     352  4  US-10-245-850-1             Sequence 1, Appli
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11	1678.5	89.9	352	4	US-10-251-703-38	Sequence 38, Appl
12	1678.5	89.9	352	4	US-10-021-660-123	Sequence 123, App
13	1678.5	89.9	352	4	US-10-014-322A-126	Sequence 126, App
14	1678.5	89.9	352	4	US-10-239-423-79	Sequence 79, Appl
15	1678.5	89.9	352	4	US-10-170-385-331	Sequence 331, App
16	1678.5	89.9	352	4	US-10-160-401-3	Sequence 3, Appli
17	1678.5	89.9	352	4	US-10-341-434-178	Sequence 178, App
18	1678.5	89.9	352	4	US-10-372-683-2	Sequence 2, Appli
19	1678.5	89.9	352	4	US-10-440-464-78	Sequence 78, Appl
20	1678.5	89.9	352	4	US-10-452-015-1	Sequence 1, Appli
21	1678.5	89.9	352	4	US-10-211-462-81	Sequence 81, Appl
22	1678.5	89.9	352	4	US-10-666-689-4	Sequence 4, Appli
23	1678.5	89.9	352	4	US-10-181-906-10	Sequence 10, Appl
24	1678.5	89.9	352	4	US-10-706-265-10	Sequence 10, Appl
25	1678.5	89.9	352	4	US-10-785-230-1	Sequence 1, Appli
26	1678.5	89.9	352	5	US-10-486-471-20	Sequence 20, Appl
27	1678.5	89.9	352	5	US-10-985-324-2	Sequence 2, Appli
28	1678.5	89.9	352	6	US-11-021-951-189	Sequence 189, App
29	1678.5	89.9	352	6	US-11-028-922A-1	Sequence 1, Appli
30	1672.5	89.6	352	3	US-09-826-509-485	Sequence 485, App
31	1672.5	89.6	352	5	US-10-925-095-485	Sequence 485, App
32	1672.5	89.6	356	5	US-10-723-860-1280	Sequence 1280, Ap
33	1670.5	89.5	352	3	US-09-870-759-37	Sequence 37, Appl
34	1670.5	89.5	352	3	US-09-870-759-144	Sequence 144, App
35	1670.5	89.5	352	3	US-09-751-708A-37	Sequence 37, Appl
36	1670.5	89.5	352	3	US-09-751-708A-144	Sequence 144, App
37	1670.5	89.5	352	4	US-10-428-817A-33	Sequence 33, Appl
38	1670.5	89.5	352	4	US-10-428-817A-140	Sequence 140, App
39	1670.5	89.5	352	5	US-10-937-758A-37	Sequence 37, Appl
40	1670.5	89.5	352	5	US-10-937-758A-121	Sequence 121, App
41	1641.5	87.9	352	5	US-10-791-592-6	Sequence 6, Appli
42	1641.5	87.9	352	5	US-10-791-166-6	Sequence 6, Appli
43	1633.5	87.5	348	5	US-10-330-773-921	Sequence 921, App
44	969.5	51.9	209	4	US-10-292-798-688	Sequence 688, App
45	964.5	51.7	209	4	US-10-017-161-790	Sequence 790, App

ALIGNMENTS

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RESULT 1
US-10-785-230-3
; Sequence 3, Application US/10785230
; Publication No. US20040209837A1
; GENERAL INFORMATION:
;  APPLICANT: KISHIMOTO, Tadamitsu
;  APPLICANT:  NAGASAWA, Takashi
;  APPLICANT:  TACHIBANA, Kazunobu
;  APPLICANT:  CHUGAI SEIYAKU KABUSIKI KAISHA
;  TITLE OF INVENTION: Vascularization Inhibitors
;  FILE REFERENCE: 46124-5042-US
;  CURRENT APPLICATION NUMBER: US/10/785,230
;  CURRENT FILING DATE:  2004-02-25
;  PRIOR APPLICATION NUMBER: PCT/JP99/01448
;  PRIOR FILING DATE: 1999-03-23
;  PRIOR APPLICATION NUMBER: JP10/95448
;  PRIOR FILING DATE: 1998-03-24
;  NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 3
;   LENGTH: 359
;   TYPE: PRT
;   ORGANISM: Mus
US-10-785-230-3

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  Matches  359;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEPISVSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGL 60
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Db          1 MEPISVSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGL 60

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Db        121 NLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVS 180

Qy        181 QGDISQGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQ 240
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Db        181 QGDISQGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQ 240

Qy        241 KRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFF 300
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Qy        301 HCCLNPILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
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Db        301 HCCLNPILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359


RESULT 2
US-10-330-773-918
; Sequence 918, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
;  APPLICANT: David W. Morris
;  APPLICANT:  Marc Malandro
;  TITLE OF INVENTION: Novel Compositions and Methods in Cancer
;  FILE REFERENCE: 529452001300
;  CURRENT APPLICATION NUMBER: US/10/330,773.
;  CURRENT FILING DATE:  2002-12-27
;  NUMBER OF SEQ ID NOS: 981
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 918
;   LENGTH: 355
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-330-773-918

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Qy        181 QGDISQGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQ 240
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Qy        241 KRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFF 300
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Qy        301 HCCLNPILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
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RESULT 3
US-11-028-922A-2
; Sequence 2, Application US/11028922A
; Publication No. US20050271639A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Marc
;  TITLE OF INVENTION: GENETICALLY ENGINEERED FOR THERAPEUTIC APPLICATIONS
;  FILE REFERENCE: CCF-7019
;  CURRENT APPLICATION NUMBER: US/11/028,922A
;  CURRENT FILING DATE:  2005-01-04
;  NUMBER OF SEQ ID NOS: 9
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;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
;   LENGTH: 349
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-11-028-922A-2

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              : |||||||||||||||||||||||||||| :|||||||||||||||||||||||||||||
Db          1 MEIYTSDNYSEEVGSGDYDSNKEPCFRDENENFNRIFLPTIYFIIFLTGIVGNGLVILVM 60

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
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Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
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Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
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RESULT 4
US-09-953-692-2
; Sequence 2, Application US/09953692
; Patent No. US20020107195A1
; GENERAL INFORMATION:
;  APPLICANT: Shalley, Gupta K.
;  TITLE OF INVENTION: Method for Inducing Chemotaxis in Endothelial Cells by
;  TITLE OF INVENTION:  Administering Stromal Cell Derived Factor-1(
;  FILE REFERENCE: P50676C1
;  CURRENT APPLICATION NUMBER: US/09/953,692
;  CURRENT FILING DATE:  2001-09-17
;  PRIOR APPLICATION NUMBER: 09/358,624
;  PRIOR FILING DATE: 1999-07-21
;  PRIOR APPLICATION NUMBER: 60/093,596
;  PRIOR FILING DATE: 1998-07-21
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Human
US-09-953-692-2

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Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              :||||||||:||:||||||| |||||||:|| :||:||||||| ||||||||||||||||
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Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
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              : |||||||| ||:. ||:|||||||||||||||||||||||||||||||||||||||||||
Db        179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 238

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
              |||||||||||||||||:||||||||| :|||||:||: ||||||||||||||||||
Db        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 298

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              ||||||||||||:|||||| |:|||||||||||||||||||||||||||||||
Db        299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 5
US-09-953-717-2
; Sequence 2, Application US/09953717
; Patent No. US20020107196A1
; GENERAL INFORMATION:
;  APPLICANT: Shalley, Gupta K.
;  TITLE OF INVENTION: Method for Inducing Chemotaxis in Endothelial Cells by
;  TITLE OF INVENTION:  Administering Stromal Cell Derived Factor-1(
;  FILE REFERENCE: P50676D1
;  CURRENT APPLICATION NUMBER: US/09/953,717
;  CURRENT FILING DATE:  2001-09-17
;  PRIOR APPLICATION NUMBER: 09/358,624
;  PRIOR FILING DATE: 1999-07-21
;  PRIOR APPLICATION NUMBER: 60/093,596
;  PRIOR FILING DATE: 1998-07-21
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Human
US-09-953-717-2

  Query Match             89.9%;  Score 1678.5;  DB 3;  Length 352;
  Best Local Similarity   90.1%;  Pred. No. 1.7e-143;
  Matches  319;  Conservative   19;  Mismatches   11;  Indels    5;  Gaps    1;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              :|||||||:||:|||||||  ||||||:|| :||:|||||||  ||||||||||||||||
Db          4 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              ||||||||||||||||||||||||||||||:|:|||| |||||||:|||||||||
Db         64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||||||||||||||||||||||||||||||||||||:|     |
Db        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 178

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              : |||||||| ||: ||:|||||||||||||||||||||||||||||||||||||||||||
Db        179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 238

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
              |||||||||||||||||:||||||||| :|||||:||: ||||||||||||||||||
Db        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 298

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              ||||||||||||:|||||| |:|||||||||||||||||||||||||||||||
Db        299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 6
US-09-104-063-4
; Sequence 4, Application US/09104063
; Patent No. US20020168356A1
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, James
;    APPLICANT:  Wood, William I.
;    TITLE OF INVENTION:  PF4A Receptors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
```

```
;       CITY:  South San Francisco
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94080
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  WinPatin (Genentech)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/104,063
;       FILING DATE:  24-June-1998
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/701265
;       FILING DATE:  22-AUG-1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/664228
;       FILING DATE:  06-JUN-1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/076093
;       FILING DATE:  11-JUN-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/810782
;       FILING DATE:  19-DEC-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Love, Richard B.
;       REGISTRATION NUMBER:  34,659
;       REFERENCE/DOCKET NUMBER:  P0706P2C2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415/225-5530
;       TELEFAX:  415/952-9881
;       TELEX:  910/371-7168
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  352 amino acids
;       TYPE:  Amino Acid
;       TOPOLOGY:  Linear
US-09-104-063-4

  Query Match             89.9%;  Score 1678.5;  DB 3;  Length 352;
  Best Local Similarity   90.1%;  Pred. No. 1.7e-143;
  Matches  319;  Conservative   19;  Mismatches   11;  Indels    5;  Gaps    1;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              :||||||||:||:||||||| ||||||:|| :||:||||||| ||||||||||||||||
Db          4 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              ||||||||||||||||||||||||||||||||||:|:|||| |||||||:|||||||||
Db         64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||||||||||||| ||||||||||||||||||:|     |
Db        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 178

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              : |||||||| ||: ||:||||||||||||||||||||||||||||||||||||||||||
Db        179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 238

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
              |||||||||||||||||:|||||||||| :|||||:||: ||||||||||||||||||
Db        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 298

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              ||||||||||||:|||||| |:||||||||||||||||||||||||||||||||
Db        299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 7
US-09-813-651B-85
; Sequence 85, Application US/09813651B
; Publication No. US20030018438A1
; GENERAL INFORMATION:
;  APPLICANT: Nestor, John
;  APPLICANT:  Wilson, Carol
```

```
;  APPLICANT:  Tan Hehir, Christina
;  APPLICANT:  Kates, Steven
;  TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compounds
;  FILE REFERENCE: CNS-007
;  CURRENT APPLICATION NUMBER: US/09/813,651B
;  CURRENT FILING DATE:  2001-03-20
;  PRIOR APPLICATION NUMBER: US 60/190,946
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: US 60/190,996
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: US 60/191,299
;  PRIOR FILING DATE: 2000-03-21
;  NUMBER OF SEQ ID NOS: 85
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 85
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-813-651B-85

  Query Match             89.9%;  Score 1678.5;  DB 3;  Length 352;
  Best Local Similarity   90.1%;  Pred. No. 1.7e-143;
  Matches  319;  Conservative   19;  Mismatches   11;  Indels    5;  Gaps    1;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              :||||||||:||:||||||| |||||:|| :||:||||||| ||||||||||||||||
Db          4 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              |||||||||||||||||||||||||||||||:|:|||| |||||||:|||||||||
Db         64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||||||||||||| ||||||||||||||||||:|     |
Db        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 178

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              : |||||||| ||: ||:||||||||||||||||||||||||||||||||||||||||||
Db        179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 238

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
              ||||||||||||||||:|||||||||| :|||||:||: ||||||||||||||||||
Db        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 298

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              |||||||||||:|||||| |:||||||||||||||||||||||||||||||||
Db        299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 8
US-10-151-274-4
; Sequence 4, Application US/10151274
; Publication No. US20030064071A1
; GENERAL INFORMATION:
;  APPLICANT: Littman, Dan R.
;  APPLICANT:  Kwon, Douglas S.
;  APPLICANT:  van Kooyk, Yvette
;  APPLICANT:  Geijtenbeck, Tneo
;  TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY
;  TITLE OF INVENTION:  INTO
;  TITLE OF INVENTION:  CELLS
;  FILE REFERENCE: 1049-1-017
;  CURRENT APPLICATION NUMBER: US/10/151,274
;  CURRENT FILING DATE:  2002-05-20
;  PRIOR APPLICATION NUMBER: US/09/517,605
;  PRIOR FILING DATE: 2000-03-02
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-151-274-4

  Query Match             89.9%;  Score 1678.5;  DB 4;  Length 352;
  Best Local Similarity   90.1%;  Pred. No. 1.7e-143;
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  Matches  319;  Conservative   19;  Mismatches   11;  Indels    5;  Gaps    1;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              :||||||||:||:||||||| |||||:|| :||:||||||| ||||||||||||||||
Db          4 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              |||||||||||||||||||||||||||||||:|:|||| |||||||:|||||||||
Db         64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||||||||||||| ||||||||||||||||||:|     |
Db        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 178

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              : |||||||| ||: ||:||||||||||||||||||||||||||||||||||||||||||
Db        179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 238

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
              ||||||||||||||||:|||||||||| :|||||:||: ||||||||||||||||||
Db        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 298

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              |||||||||||:|||||| |:||||||||||||||||||||||||||||||
Db        299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 9
US-10-225-567A-76
; Sequence 76, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
;  APPLICANT: LifeSpan Biosciences
;  APPLICANT:  Brown, Joseph P.
;  APPLICANT:  Burmer, Glenna C.
;  APPLICANT:  Roush, Christine L.
;  TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS (GPCRS)
;  FILE REFERENCE: 1920-4-4
;  CURRENT APPLICATION NUMBER: US/10/225,567A
;  CURRENT FILING DATE:  2001-12-19
;  PRIOR APPLICATION NUMBER: 60/257,144
;  PRIOR FILING DATE: 2000-12-19
;  NUMBER OF SEQ ID NOS: 2292
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-225-567A-76

  Query Match             89.9%;  Score 1678.5;  DB 4;  Length 352;
  Best Local Similarity   90.1%;  Pred. No. 1.7e-143;
  Matches  319;  Conservative   19;  Mismatches   11;  Indels    5;  Gaps    1;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              :||||||||:||:||||||| |||||:|| :||:||||||| ||||||||||||||||
Db          4 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              |||||||||||||||||||||||||||||||:|:|||| |||||||:|||||||||
Db         64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||||||||||||| ||||||||||||||||||:|     |
Db        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 178

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              : |||||||| ||: ||:||||||||||||||||||||||||||||||||||||||||||
Db        179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 238

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
              ||||||||||||||||:|||||||||| :|||||:||: ||||||||||||||||||.
Db        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 298

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              |||||||||||:|||||| |:||||||||||||||||||||||||||||||
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Db        299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 10
US-10-245-850-1
; Sequence 1, Application US/10245850
; Publication No. US20030124628A1
; GENERAL INFORMATION:
;  APPLICANT: Burns, Jennifer M.
;  APPLICANT:  Miao, Zhenhua
;  APPLICANT:  Wei, Zheng
;  APPLICANT:  Howard, Maureen C.
;  APPLICANT:  Premack, Brett A.
;  APPLICANT:  Schall, Thomas J.
;  APPLICANT:  ChemoCentryx, Inc.
;  TITLE OF INVENTION: Compositions and Methods for Detecting and Treating
;  TITLE OF INVENTION:  Diseases and Conditions Related to Chemokine Receptors
;  FILE REFERENCE: 019934-003310US
;  CURRENT APPLICATION NUMBER: US/10/245,850
;  CURRENT FILING DATE:  2002-09-16
;  PRIOR APPLICATION NUMBER: US 60/338,100
;  PRIOR FILING DATE: 2001-11-30
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: CXCR4 chemokine receptor
US-10-245-850-1

  Query Match             89.9%;  Score 1678.5;  DB 4;  Length 352;
  Best Local Similarity   90.1%;  Pred. No. 1.7e-143;
  Matches  319;  Conservative   19;  Mismatches   11;  Indels    5;  Gaps    1;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              :||||||||:||:||||||| ||||||:|| :||:||||||| ||||||||||||||||
Db          4 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              |||||||||||||||||||||||||||||||:|:|||| |||||||:|||||||||
Db         64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||||||||||||| ||||||||||||||||||:|     |
Db        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 178

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              : |||||||| ||: ||:||||||||||||||||||||||||||||||||||||||||||
Db        179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 238

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
              |||||||||||||||:|||||||||| :|||||:||: ||||||||||||||||||
Db        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 298

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              ||||||||||||:|||||| |:|||||||||||||||||||||||||||||||
Db        299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 11
US-10-251-703-38
; Sequence 38, Application US/10251703
; Publication No. US20030148449A1
; GENERAL INFORMATION:
;  APPLICANT: Kuliopulos, Athan
;  APPLICANT:  Covic, Lidija
;  TITLE OF INVENTION: G Protein Coupled Receptor Agonists and Antagonists and
;  TITLE OF INVENTION:  Methods of Activating and Inhibiting G Protein Coupled
;  TITLE OF INVENTION:  Receptors Using the Same
;  FILE REFERENCE: NEMC-215 CIP
;  CURRENT APPLICATION NUMBER: US/10/251,703
;  CURRENT FILING DATE:  2002-09-20
;  PRIOR APPLICATION NUMBER: 09/841,091
;  PRIOR FILING DATE: 2001-04-23
```

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;  PRIOR APPLICATION NUMBER: 60/198,993
;  PRIOR FILING DATE: 2000-04-21
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Pepducin
;   OTHER INFORMATION: Peptide Sequence
US-10-251-703-38

  Query Match             89.9%;  Score 1678.5;  DB 4;  Length 352;
  Best Local Similarity   90.1%;  Pred. No. 1.7e-143;
  Matches  319;  Conservative   19;  Mismatches   11;  Indels    5;  Gaps    1;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              :||||||||:||:||||||| ||||||:|| :||:||||||| ||||||||||||||||
Db          4 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              ||||||||||||||||||||||||||||||||:|:|||| |||||||:||||||||
Db         64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||||||||||| ||||||||||||||||||:|     |
Db        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 178

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              : |||||||| ||: ||:||||||||||||||||||||||||||||||||||||||||
Db        179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 238

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
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Db        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 298

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
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Db        299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 12
US-10-021-660-123
; Sequence 123, Application US/10021660
; Publication No. US20030152926A1
; GENERAL INFORMATION:
;  APPLICANT: Murray, Richard
;  APPLICANT:  Glynne, Richard
;  APPLICANT:  Watson, Susan R.
;  APPLICANT:  EOS Biotechnology, Inc.
;  TITLE OF INVENTION: No. US20030152926A1el Methods of Diagnosis of Angiogenesis,
;  TITLE OF INVENTION:  Compositions and Methods of Screening for Angiogenesis
;  TITLE OF INVENTION:  Modulators
;  FILE REFERENCE: 018501-000710US
;  CURRENT APPLICATION NUMBER: US/10/021,660
;  CURRENT FILING DATE:  2001-12-06
;  PRIOR APPLICATION NUMBER: US/09/784,356
;  PRIOR FILING DATE: 2001-02-14
;  PRIOR APPLICATION NUMBER: US 09/637,977
;  PRIOR FILING DATE: 2000-08-11
;  NUMBER OF SEQ ID NOS: 135
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 123
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-021-660-123

  Query Match             89.9%;  Score 1678.5;  DB 4;  Length 352;
  Best Local Similarity   90.1%;  Pred. No. 1.7e-143;
  Matches  319;  Conservative   19;  Mismatches   11;  Indels    5;  Gaps    1;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
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Db          4 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63
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Qy          66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
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Db          64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy         126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
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Db         124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 178

Qy         186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
               : |||||||| ||: ||:||||||||||||||||||||||||||||||||||||||||||
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Qy         246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
               |||||||||||||||||:|||||||||| :|||||:||: ||||||||||||||||||
Db         239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 298

Qy         306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
               ||||||||||||:|||||| |:||||||||||||||||||||||||||||||
Db         299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 13
US-10-014-322A-126
; Sequence 126, Application US/10014322A
; Publication No. US20030167129A1
; GENERAL INFORMATION:
;  APPLICANT: Nestor, Jr., John
;  APPLICANT:  Wilson, Carol
;  APPLICANT:  Tan Hehir, Christina
;  APPLICANT:  Kates, Steven
;  APPLICANT:  Krstenansky, John
;  TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compounds
;  FILE REFERENCE: CNS-008
;  CURRENT APPLICATION NUMBER: US/10/014,322A
;  CURRENT FILING DATE:  2002-07-08
;  PRIOR APPLICATION NUMBER: US 60/243,587
;  PRIOR FILING DATE: 2000-10-27
;  PRIOR APPLICATION NUMBER: US 09/813,651
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: US 09/813,653
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: US 09/813,448
;  PRIOR FILING DATE: 2001-03-20
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 126
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-014-322A-126

  Query Match             89.9%;  Score 1678.5;  DB 4;  Length 352;
  Best Local Similarity   90.1%;  Pred. No. 1.7e-143;
  Matches  319;  Conservative   19;  Mismatches   11;  Indels    5;  Gaps    1;

Qy           6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
               :||||||||:||:||||||| ||||||:|| :||:||||||| ||||||||||||||||
Db           4 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy          66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
               ||||||||||||||||||||||||||||||||||:|:|||| |||||||:|||||||||
Db          64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy         126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
               |||||||||||||||||||||||||||||| ||||||||||||||||||:|     |
Db         124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 178

Qy         186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
               : |||||||| ||: ||:||||||||||||||||||||||||||||||||||||||||||
Db         179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 238

Qy         246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
               |||||||||||||||||:|||||||||| :|||||:||: ||||||||||||||||||
Db         239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 298
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Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              ||||||||||||:|||||| |:||||||||||||||||||||||||||||||||
Db        299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 14
US-10-239-423-79
; Sequence 79, Application US/10239423
; Publication No. US20030186889A1
; GENERAL INFORMATION:
;  APPLICANT: FORSSMANN, Wolf-Georg; FORSSMANN, Ulf; ADERMANN, Knut;
;  APPLICANT:  HEITLAND, Aleksandra; SPODSBERG, Nikolaj
;  TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
;  TITLE OF INVENTION:  Cell Surface Proteome of Tumor and Inflammation Cells and
;  TITLE OF INVENTION:  for Treating Tumor Diseases and Inflammatory Diseases,
;  TITLE OF INVENTION:  Preferably with the Aid of Specific Chemokine
;  TITLE OF INVENTION:  Receptor Analysis and Chemokine Receptor/Ligand Interaction
;  FILE REFERENCE: 022217us
;  CURRENT APPLICATION NUMBER: US/10/239,423
;  CURRENT FILING DATE:  2002-09-23
;  PRIOR APPLICATION NUMBER: DE10016013.1
;  PRIOR FILING DATE: 2000-03-31
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
US-10-239-423-79

  Query Match             89.9%;  Score 1678.5;  DB 4;  Length 352;
  Best Local Similarity   90.1%;  Pred. No. 1.7e-143;
  Matches  319;  Conservative   19;  Mismatches   11;  Indels    5;  Gaps    1;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              :|||||||:||:||||||| |||||:|| :||:||||||| ||||||||||||||||
Db          4 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              ||||||||||||||||||||||||||||||||:|:|||| |||||||:|||||||||
Db         64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||||||||||||| ||||||||||||||||||:|     |
Db        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 178

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
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Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
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Db        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 298

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
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RESULT 15
US-10-170-385-331
; Sequence 331, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
;  APPLICANT: Ward, Neil Raymond
;  APPLICANT:  Mundy, Christopher Robert
;  APPLICANT:  Kan, On
;  APPLICANT:  Harris, Robert Alan
;  APPLICANT:  White, Jonathan
;  APPLICANT:  Binley, Katie Mary
;  APPLICANT:  Rayner, William Nigel
;  APPLICANT:  Naylor, Stuart
;  APPLICANT:  Kingsman, Susan Mary
```

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;  APPLICANT:  Krige, David
;  TITLE OF INVENTION: ANALYSIS METHOD
;  FILE REFERENCE: 532682000100
;  CURRENT APPLICATION NUMBER: US/10/170,385
;  CURRENT FILING DATE:  2002-06-12
;  PRIOR APPLICATION NUMBER: PCT/GB02/01662
;  PRIOR FILING DATE: 2002-04-08
;  PRIOR APPLICATION NUMBER: PCT/GB01/05458
;  PRIOR FILING DATE: 2001-12-10
;  NUMBER OF SEQ ID NOS: 549
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 331
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-170-385-331

  Query Match             89.9%;  Score 1678.5;  DB 4;  Length 352;
  Best Local Similarity   90.1%;  Pred. No. 1.7e-143;
  Matches  319;  Conservative   19;  Mismatches   11;  Indels    5;  Gaps    1;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              :||||||||:||:|||||||  ||||||:||  :||:||||||| |||||||||||||||
Db          4 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              ||||||||||||||||||||||||||||||||:|:|||| |||||||:|||||||||
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Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
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Db        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 178

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              : |||||||| ||: ||:||||||||||||||||||||||||||||||||||||||||||
Db        179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 238

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
              ||||||||||||||||:|||||||||| :|||||:||: ||||||||||||||||||
Db        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 298

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
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Db        299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


Search completed: February  6, 2007, 14:29:55
Job time : 137.834 secs
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SCORE 1.3 BuildDate: 11/17/2006

SCORE Search Results Details for Application 10785230 and Search Result 20070206_074037_us-10-785-230-3.rapbn.

This page gives you Search Results detail for the Application 10785230 and Search Result 20070206_074037_us-10-785-230-3.rapbn.

start

Go Back to previous page

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                          GenCore version 6.2
                 Copyright (c) 1993 - 2007  Biocceleration Ltd.


OM protein - protein search, using sw model

Run on:          February  6, 2007, 14:25:40 ; Search time 41 Seconds
                                          (without alignments)
                                          1194.020 Million cell updates/sec

Title:           US-10-785-230-3
Perfect score:   1867
Sequence:        1 MEPISVSIYTSDNYSEEVGS.........KRGGHSSVSTESESSSFHSS 359

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        571941 seqs, 137706945 residues

Total number of hits satisfying chosen parameters:      571941

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        Published_Applications_AA_New:*
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                 2:  /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
                 3:  /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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                 7:  /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
                 8:  /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                    SUMMARIES

                    %
Result              Query
   No.    Score     Match  Length  DB  ID                          Description
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     1     1867    100.0     359   7  US-11-437-734-2              Sequence 2, Appli
     2     1834     98.2     352   7  US-11-437-734-8              Sequence 8, Appli
     3     1822     97.6     355   6  US-10-540-898-918            Sequence 918, App
     4   1744.5     93.4     349   6  US-10-219-051B-9076.         Sequence 9076, Ap
     5   1744.5     93.4     349   6  US-10-219-051B-9080          Sequence 9080, Ap
     6   1678.5     89.9     352   6  US-10-505-928-745            Sequence 745, App
     7   1678.5     89.9     352   6  US-10-511-937-2486           Sequence 2486, Ap
     8   1678.5     89.9     352   6  US-10-511-937-2935           Sequence 2935, Ap
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9	1678.5	89.9	352	6	US-10-511-937-3010	Sequence 3010, Ap
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11	1678.5	89.9	352	6	US-10-219-051B-9082	Sequence 9082, Ap
12	1678.5	89.9	352	7	US-11-371-354-68409	Sequence 68409, A
13	1678.5	89.9	363	6	US-10-545-557-19	Sequence 19, Appl
14	1672.5	89.6	352	7	US-11-404-939-485	Sequence 485, App
15	1633.5	87.5	348	6	US-10-540-898-921	Sequence 921, App
16	1210	64.8	230	7	US-11-437-734-4	Sequence 4, Appli
17	974	52.2	188	7	US-11-437-734-6	Sequence 6, Appli
18	969.5	51.9	209	7	US-11-214-063A-688	Sequence 688, App
19	584	31.3	368	6	US-10-511-937-2505	Sequence 2505, Ap
20	584	31.3	368	6	US-10-511-937-2931	Sequence 2931, Ap
21	584	31.3	368	7	US-11-302-678-59	Sequence 59, Appl
22	584	31.3	368	7	US-11-371-354-63307	Sequence 63307, A
23	570.5	30.6	360	6	US-10-581-413-1	Sequence 1, Appli
24	562.5	30.1	361	6	US-10-669-920-374	Sequence 374, App
25	562	30.1	359	6	US-10-219-051B-13793	Sequence 13793, A
26	551	29.5	364	6	US-10-669-920-377	Sequence 377, App
27	544.5	29.2	360	6	US-10-533-519-1184	Sequence 1184, Ap
28	544.5	29.2	360	6	US-10-219-051B-13795	Sequence 13795, A
29	544.5	29.2	360	7	US-11-242-111-19	Sequence 19, Appl
30	544.5	29.2	360	7	US-11-371-354-67277	Sequence 67277, A
31	537.5	28.8	374	6	US-10-669-920-3	Sequence 3, Appli
32	537.5	28.8	378	6	US-10-511-937-2404	Sequence 2404, Ap
33	537.5	28.8	389	6	US-10-545-557-23	Sequence 23, Appl
34	537.5	28.8	475	7	US-11-520-715-56811	Sequence 56811, A
35	534	28.6	357	7	US-11-371-354-66939	Sequence 66939, A
36	534	28.6	369	7	US-11-371-354-69405	Sequence 69405, A
37	533	28.5	355	6	US-10-516-032-8	Sequence 8, Appli
38	533	28.5	355	6	US-10-533-519-1109	Sequence 1109, Ap
39	533	28.5	355	7	US-11-371-354-56785	Sequence 56785, A
40	532	28.5	367	7	US-11-392-789-2	Sequence 2, Appli
41	528	28.3	369	7	US-11-404-939-481	Sequence 481, App
42	525.5	28.1	350	7	US-11-371-354-61621	Sequence 61621, A
43	522.5	28.0	350	7	US-11-371-354-68399	Sequence 68399, A
44	519.5	27.8	374	6	US-10-669-920-6	Sequence 6, Appli
45	512.5	27.5	325	6	US-10-669-920-237	Sequence 237, App

ALIGNMENTS

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RESULT 1
US-11-437-734-2
; Sequence 2, Application US/11437734
; Publication No. US20060211037A1
; GENERAL INFORMATION:
;  APPLICANT: KISHIMOTO, Tadamitsu
;  APPLICANT:  NAGASAWA, Takashi
;  APPLICANT:  TACHIBANA, Kazunobu
;  APPLICANT:  IIZASA, Hisashi
;  APPLICANT:  YOSHIDA, Nobuaki
;  APPLICANT:  NAKAJIMA, Toshihiro
;  APPLICANT:  YOSHIE, Osamu
;  TITLE OF INVENTION: NOVEL MOUSE CXC CHEMOKINE RECEPTOR
;  FILE REFERENCE: 1422-386P
;  CURRENT APPLICATION NUMBER: US/11/437,734
;  CURRENT FILING DATE:  2006-05-22
;  PRIOR APPLICATION NUMBER: US/09/367,052
;  PRIOR FILING DATE: 1999-08-06
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 359
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-11-437-734-2

  Query Match             100.0%;  Score 1867;  DB 7;  Length 359;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-168;
  Matches  359;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEPISVSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGL 60
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Qy        121 NLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVS 180
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Qy        181 QGDISQGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQ 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 QGDISQGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQ 240

Qy        241 KRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFF 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 KRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFF 300

Qy        301 HCCLNPILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 HCCLNPILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359


RESULT 2
US-11-437-734-8
; Sequence 8, Application US/11437734
; Publication No. US20060211037A1
; GENERAL INFORMATION:
;  APPLICANT: KISHIMOTO, Tadamitsu
;  APPLICANT:  NAGASAWA, Takashi
;  APPLICANT:  TACHIBANA, Kazunobu
;  APPLICANT:  IIZASA, Hisashi
;  APPLICANT:  YOSHIDA, Nobuaki
;  APPLICANT:  NAKAJIMA, Toshihiro
;  APPLICANT:  YOSHIE, Osamu
;  TITLE OF INVENTION: NOVEL MOUSE CXC CHEMOKINE RECEPTOR
;  FILE REFERENCE: 1422-386P
;  CURRENT APPLICATION NUMBER: US/11/437,734
;  CURRENT FILING DATE:  2006-05-22
;  PRIOR APPLICATION NUMBER: US/09/367,052
;  PRIOR FILING DATE: 1999-08-06
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-11-437-734-8

  Query Match             98.2%;  Score 1834;  DB 7;  Length 352;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-165;
  Matches  352;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 IYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVMGY 67
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 IYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVMGY 60

Qy         68 QKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSSVL 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 QKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSSVL 120

Qy        128 ILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDISQG 187
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDISQG 180

Qy        188 DDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKT 240

Qy        248 TVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLNPI 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLNPI 300

Qy        308 LYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
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```
RESULT 3
US-10-540-898-918
; Sequence 918, Application US/10540898
; Publication No. US20060166213A1
; GENERAL INFORMATION:
;  APPLICANT: David W. Morris
;  APPLICANT:  Marc Malandro
;  TITLE OF INVENTION: Novel Compositions and Methods in Cancer
;  FILE REFERENCE: CHIR0056-101 (PP023367.0003)
;  CURRENT APPLICATION NUMBER: US/10/540,898
;  CURRENT FILING DATE:  2005-06-27
;  PRIOR APPLICATION NUMBER: US 10/330,773
;  PRIOR FILING DATE: 2002-12-27
;  NUMBER OF SEQ ID NOS: 981
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 918
;   LENGTH: 355
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-540-898-918

  Query Match             97.6%;  Score 1822;  DB 6;  Length 355;
  Best Local Similarity   98.6%;  Pred. No. 2e-164;
  Matches  354;  Conservative    0;  Mismatches    1;  Indels    4;  Gaps    2;

Qy          1 MEPISVSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEPISVSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGL 60

Qy         61 VILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 VILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTV 120

Qy        121 NLYSSVLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVS 180
              |   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 N--KSVLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVS 178

Qy        181 QGDISQGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQ 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 QGDISQGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQ 238

Qy        241 KRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFF 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        239 KRKALKTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITE--AFF 296

Qy        301 HCCLNPILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        297 HCCLNPILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 355


RESULT 4
US-10-219-051B-9076
; Sequence 9076, Application US/10219051B
; Publication No. US20070015145A1
; GENERAL INFORMATION:
;  APPLICANT: The General Hospital Corporation doing business as Massachusetts General
;  APPLICANT:  Hospital / Bayer AG
;  TITLE OF INVENTION: Nucleotide sequences involved in pain
;  FILE REFERENCE: LeA 35693 Foreign Countries
;  CURRENT APPLICATION NUMBER: US/10/219,051B
;  CURRENT FILING DATE:  2003-05-09
;  PRIOR APPLICATION NUMBER: US 60/312,147
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/346,382
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: US 60/333,347
;  PRIOR FILING DATE: 2001-11-26
;  NUMBER OF SEQ ID NOS: 14715
;  SOFTWARE: Perl script
; SEQ ID NO 9076
;   LENGTH: 349
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: SWISS-Prot / O08565
;   DATABASE ENTRY DATE: 2001-10-16
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US-10-219-051B-9076

Query Match 93.4%; Score 1744.5; DB 6; Length 349;
Best Local Similarity 95.5%; Pred. No. 4.2e-157;
Matches 338; Conservative 4; Mismatches 7; Indels 5; Gaps 1;

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Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              : ||||||||||||||||||||||||||||| :|||||||||||||||||||||||||||||
Db          1 MEIYTSDNYSEEVGSGDYDSNKEPCFRDENENFNRIFLPTIYFIIFLTGIVGNGLVILVM 60

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 120

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||||  |||||||||||||||||||||||| |||||     |
Db        121 VLILAFISLDRYLAIVHATNSQSARKLLAEKAVYVGVWIPALLLTIPDIIFADV-----S 175

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 QGDGRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 235

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
              |||||||||||||||||||||||||||| |||||:|||:||||||||||||||||||||
Db        236 KTTVILILAFFACWLPYYVGISIDSFILLEVIKQGCEFESVVHKWISITEALAFFHCCLN 295

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 349
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RESULT 5
US-10-219-051B-9080
; Sequence 9080, Application US/10219051B
; Publication No. US20070015145A1
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: LeA 35693 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/219,051B
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/312,147
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/346,382
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/333,347
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 14715
; SOFTWARE: Perl script
; SEQ ID NO 9080
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SWISS-Prot / O08565
; DATABASE ENTRY DATE: 2001-10-16
US-10-219-051B-9080

Query Match 93.4%; Score 1744.5; DB 6; Length 349;
Best Local Similarity 95.5%; Pred. No. 4.2e-157;
Matches 338; Conservative 4; Mismatches 7; Indels 5; Gaps 1;

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Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              : ||||||||||||||||||||||||||||| :|||||||||||||||||||||||||||||
Db          1 MEIYTSDNYSEEVGSGDYDSNKEPCFRDENENFNRIFLPTIYFIIFLTGIVGNGLVILVM 60

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 120

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||||  |||||||||||||||||||||||| |||||     |
Db        121 VLILAFISLDRYLAIVHATNSQSARKLLAEKAVYVGVWIPALLLTIPDIIFADV-----S 175

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
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                ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 QGDGRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 235

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
                |||||||||||||||||||||||||||||| |||||:|||:||||||||||||||||||
Db        236 KTTVILILAFFACWLPYYVGISIDSFILLEVIKQGCEFESVVHKWISITEALAFFHCCLN 295

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 349


RESULT 6
US-10-505-928-745
; Sequence 745, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
;  APPLICANT: Ludwig Institute for Cancer Research et al.
;  TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
;  FILE REFERENCE: 28967/39178
;  CURRENT APPLICATION NUMBER: US/10/505,928
;  CURRENT FILING DATE:  2004-08-27
;  PRIOR APPLICATION NUMBER: US 60/363,019
;  PRIOR FILING DATE: 2002-03-07
;  NUMBER OF SEQ ID NOS: 866
;  SOFTWARE: PatentIn 3.2
; SEQ ID NO 745
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-505-928-745

  Query Match             89.9%;  Score 1678.5;  DB 6;  Length 352;
  Best Local Similarity   90.1%;  Pred. No. 7.6e-151;
  Matches  319;  Conservative   19;  Mismatches   11;  Indels    5;  Gaps    1;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              :||||||||:||:||||||| ||||||:|| :||:||||||| ||||||||||||||||
Db          4 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              ||||||||||||||||||||||||||||||||:|:|||| |||||||:|||||||||
Db         64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||||||||||||| ||||||||||||||||||:|     |
Db        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 178

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              : |||||||| ||: ||:||||||||||||||||||||||||||||||||||||||||||
Db        179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 238

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
              ||||||||||||||||:|||||||||| :||||:||: ||||||||||||||||||||
Db        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 298

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              |||||||||||:|||||| |:||||||||||||||||||||||||||||||||||
Db        299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 7
US-10-511-937-2486
; Sequence 2486, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
;  APPLICANT: EXPRESSION DIAGNOSTICS, INC.
;  APPLICANT:  Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  APPLICANT:  Prentice, James
;  APPLICANT:  Morris, MacDonald
;  APPLICANT:  Rosenberg, Steven
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
;  TITLE OF INVENTION:  AND MONITORING TRANSPLANT REJECTION
```

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;  FILE REFERENCE: 506612000104
;  CURRENT APPLICATION NUMBER: US/10/511,937
;  CURRENT FILING DATE:  2004-10-19
;  PRIOR APPLICATION NUMBER: PCT/US2003/012946
;  PRIOR FILING DATE: 2003-04-24
;  PRIOR APPLICATION NUMBER: US 10/131,831
;  PRIOR FILING DATE: 2002-04-24
;  PRIOR APPLICATION NUMBER: US 10/325,899
;  PRIOR FILING DATE: 2002-12-20
;  NUMBER OF SEQ ID NOS: 3117
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2486
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-511-937-2486

  Query Match             89.9%;  Score 1678.5;  DB 6;  Length 352;
  Best Local Similarity   90.1%;  Pred. No. 7.6e-151;
  Matches  319;  Conservative   19;  Mismatches   11;  Indels    5;  Gaps    1;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              :||||||||:||:||||||| |||||:|| :||:||||||| |||||||||||||||||
Db          4 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              ||||||||||||||||||||||||||||||||:|:|||| |||||||:|||||||||
Db         64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||||||||||||| ||||||||||||||||||:|     |
Db        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 178

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              : |||||||| ||: ||:||||||||||||||||||||||||||||||||||||||||||
Db        179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 238

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
              ||||||||||||||||:|||||||||| :|||||:||: ||||||||||||||||||
Db        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 298

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              |||||||||||:|||||| |:||||||||||||||||||||||||||||||||
Db        299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 8
US-10-511-937-2935
; Sequence 2935, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
;  APPLICANT: EXPRESSION DIAGNOSTICS, INC.
;  APPLICANT:  Wohlgemuth, Jay
;  APPLICANT:  Fry, Kirk
;  APPLICANT:  Woodward, Robert
;  APPLICANT:  Ly, Ngoc
;  APPLICANT:  Prentice, James
;  APPLICANT:  Morris, MacDonald
;  APPLICANT:  Rosenberg, Steven
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
;  TITLE OF INVENTION:  AND MONITORING TRANSPLANT REJECTION
;  FILE REFERENCE: 506612000104
;  CURRENT APPLICATION NUMBER: US/10/511,937
;  CURRENT FILING DATE:  2004-10-19
;  PRIOR APPLICATION NUMBER: PCT/US2003/012946
;  PRIOR FILING DATE: 2003-04-24
;  PRIOR APPLICATION NUMBER: US 10/131,831
;  PRIOR FILING DATE: 2002-04-24
;  PRIOR APPLICATION NUMBER: US 10/325,899
;  PRIOR FILING DATE: 2002-12-20
;  NUMBER OF SEQ ID NOS: 3117
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2935
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
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US-10-511-937-2935

Query Match 89.9%; Score 1678.5; DB 6; Length 352;
Best Local Similarity 90.1%; Pred. No. 7.6e-151;
Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;

```
Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              :|||||||||:||:||||||| |||||||:|| :||:||||||| |||||||||||||||||
Db          4 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              |||||||||||||||||||||||||||||||||:|:|||| ||||||||:|||||||||
Db         64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||||||||||||| ||||||||||||||||||:|     |
Db        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 178

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              : |||||||| ||: ||:|||||||||||||||||||||||||||||||||||||||||||
Db        179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 238

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
              ||||||||||||||||:|||||||||| :|||||:||: ||||||||||||||||||||
Db        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 298

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              |||||||||||:|||||| |:|||||||||||||||||||||||||||||||||
Db        299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
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RESULT 9
US-10-511-937-3010
; Sequence 3010, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3010
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-3010

Query Match 89.9%; Score 1678.5; DB 6; Length 352;
Best Local Similarity 90.1%; Pred. No. 7.6e-151;
Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;

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Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
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Db          4 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              |||||||||||||||||||||||||||||||||:|:|||| ||||||||:|||||||||
Db         64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
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Db        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 178

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
Db        179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 238

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
Db        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 298

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
Db        299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 10
US-10-219-051B-9078
; Sequence 9078, Application US/10219051B
; Publication No. US20070015145A1
; GENERAL INFORMATION:
;  APPLICANT: The General Hospital Corporation doing business as Massachusetts General
;  APPLICANT:  Hospital / Bayer AG
;  TITLE OF INVENTION: Nucleotide sequences involved in pain
;  FILE REFERENCE: LeA 35693 Foreign Countries
;  CURRENT APPLICATION NUMBER: US/10/219,051B
;  CURRENT FILING DATE:  2003-05-09
;  PRIOR APPLICATION NUMBER: US 60/312,147
;  PRIOR FILING DATE: 2001-08-14
;  PRIOR APPLICATION NUMBER: US 60/346,382
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: US 60/333,347
;  PRIOR FILING DATE: 2001-11-26
;  NUMBER OF SEQ ID NOS: 14715
;  SOFTWARE: Perl script
; SEQ ID NO 9078
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: SWISS-Prot / P30991
;   DATABASE ENTRY DATE: 2002-06-15
US-10-219-051B-9078

  Query Match             89.9%;  Score 1678.5;  DB 6;  Length 352;
  Best Local Similarity   90.1%;  Pred. No. 7.6e-151;
  Matches  319;  Conservative   19;  Mismatches   11;  Indels    5;  Gaps    1;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
Db          4 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
Db         64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
Db        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 178

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
Db        179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 238

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
Db        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 298

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
Db        299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 11
US-10-219-051B-9082
; Sequence 9082, Application US/10219051B
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; Publication No. US20070015145A1
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: LeA 35693 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/219,051B
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/312,147
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/346,382
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/333,347
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 14715
; SOFTWARE: Perl script
; SEQ ID NO 9082
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SWISS-Prot / P30991
; DATABASE ENTRY DATE: 2002-06-15
US-10-219-051B-9082

Query Match 89.9%; Score 1678.5; DB 6; Length 352;
Best Local Similarity 90.1%; Pred. No. 7.6e-151;
Matches 319; Conservative 19; Mismatches 11; Indels 5; Gaps 1;

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Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              :|||||||||:||:|||||||  |||||||:||  :||:|||||||  ||||||||||||||||
Db          4 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              |||||||||||||||||||||||||||||||||||:|:|||| |||||||:|||||||||
Db         64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||||||||||||| ||||||||||||||||||:|     |
Db        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 178

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              : |||||||| ||: ||:||||||||||||||||||||||||||||||||||||||||||
Db        179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 238

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
              ||||||||||||||||:|||||||||| :|||||:||: ||||||||||||||||||||
Db        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 298

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              ||||||||||||:|||||| |:|||||||||||||||||||||||||||||||||
Db        299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352
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RESULT 12
US-11-371-354-68409
; Sequence 68409, Application US/11371354
; Publication No. US20060275794A1
; GENERAL INFORMATION:
; APPLICANT: CARRINO, JOHN
; APPLICANT: LIANG, FENG
; TITLE OF INVENTION: COLLECTIONS OF MATCHED BIOLOGICAL REAGENTS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING MATCHED REAGENTS
; FILE REFERENCE: INV-1005-UT2
; CURRENT APPLICATION NUMBER: US/11/371,354
; CURRENT FILING DATE: 2006-03-07
; PRIOR APPLICATION NUMBER: 60/673,045
; PRIOR FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: 60/665,199
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/665,200
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/659,493
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/659,492
; PRIOR FILING DATE: 2005-03-07

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;  PRIOR APPLICATION NUMBER: 60/953,586
;  PRIOR FILING DATE: 2005-02-15
;  PRIOR APPLICATION NUMBER: 60/651,390
;  PRIOR FILING DATE: 2005-02-08
;  NUMBER OF SEQ ID NOS: 78682
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 68409
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-371-354-68409

  Query Match             89.9%;  Score 1678.5;  DB 7;  Length 352;
  Best Local Similarity   90.1%;  Pred. No. 7.6e-151;
  Matches  319;  Conservative   19;  Mismatches   11;  Indels    5;  Gaps    1;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              :||||||||:||:|||||||  ||||||:||  :||:|||||||  ||||||||||||||||
Db          4 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              ||||||||||||||||||||||||||||||||:|:|||| |||||||:|||||||||
Db         64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||||||||||||| ||||||||||||||||||:|      |
Db        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 178

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              : |||||||| ||: ||:||||||||||||||||||||||||||||||||||||||||||
Db        179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 238

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
              ||||||||||||||||||:|||||||||| :|||||:||: ||||||||||||||||||
Db        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 298

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              ||||||||||||:|||||| |:||||||||||||||||||||||||||||||||
Db        299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 13
US-10-545-557-19
; Sequence 19, Application US/10545557
; Publication No. US20060222654A1
; GENERAL INFORMATION:
;  APPLICANT: ANOSYS
;  TITLE OF INVENTION: METHODS AND COMPOUNDS FOR RAISING ANTIBODIES AND FOR SCREENING ANTIBODY
;  TITLE OF INVENTION:  REPERTOIRES
;  FILE REFERENCE: 3665-158
;  CURRENT APPLICATION NUMBER: US/10/545,557
;  CURRENT FILING DATE:  2005-08-15
;  PRIOR APPLICATION NUMBER: PCT/IB2004/000888
;  PRIOR FILING DATE: 2004-02-13
;  PRIOR APPLICATION NUMBER: US60/447,291
;  PRIOR FILING DATE: 2003-02-14
;  NUMBER OF SEQ ID NOS: 86
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 363
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: CXCR4 + HA Tag
US-10-545-557-19

  Query Match             89.9%;  Score 1678.5;  DB 6;  Length 363;
  Best Local Similarity   90.1%;  Pred. No. 7.9e-151;
  Matches  319;  Conservative   19;  Mismatches   11;  Indels    5;  Gaps    1;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              :||||||||:||:|||||||  ||||||:||  :||:|||||||  ||||||||||||||||
Db         15 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 74

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
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Db         75 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 134

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||||||||||||| ||||||||||||||||||||:|     |
Db        135 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 189

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              : |||||||| ||: ||:||||||||||||||||||||||||||||||||||||||||||
Db        190 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 249

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
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Db        250 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 309

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              ||||||||||||:|||||| |:||||||||||||||||||||||||||||||
Db        310 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 363


RESULT 14
US-11-404-939-485
; Sequence 485, Application US/11404939
; Publication No. US20060183164A1
; GENERAL INFORMATION:
;  APPLICANT: Lehmann-Bruinsma, Karin
;  APPLICANT:  Liaw, Chen W.
;  APPLICANT:  Lin, I-Lin
;  TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Known G
;  TITLE OF INVENTION:  Protein-Coupled Receptors
;  FILE REFERENCE: AREN-207
;  CURRENT APPLICATION NUMBER: US/11/404,939
;  CURRENT FILING DATE:  2006-04-14
;  PRIOR APPLICATION NUMBER: US/09/826,509
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/195,747
;  PRIOR FILING DATE: 2000-04-07
;  PRIOR APPLICATION NUMBER: 09/170,496
;  PRIOR FILING DATE: 1998-10-13
;  NUMBER OF SEQ ID NOS: 589
;  SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 485
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-404-939-485

  Query Match             89.6%;  Score 1672.5;  DB 7;  Length 352;
  Best Local Similarity   89.8%;  Pred. No. 2.8e-150;
  Matches  318;  Conservative   19;  Mismatches   12;  Indels    5;  Gaps    1;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
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Db          4 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              |||||||||||||||||||||||||||||||:|:|||| |||||||:||||||||
Db         64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSS 123

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||||||||||||| ||||||||||||||||||||:|     |
Db        124 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 178

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              : |||||||| ||: ||:||||||||||||||||||||||||||||||||||||||||||
Db        179 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAK 238

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
              |||||||||||||||||:|||||||||| :|||||:||: ||||||||||||||||||
Db        239 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLN 298

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              ||||||||||||:|||||| |:||||||||||||||||||||||||||||||
Db        299 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 352


RESULT 15
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US-10-540-898-921
; Sequence 921, Application US/10540898
; Publication No. US20060166213A1
; GENERAL INFORMATION:
;  APPLICANT: David W. Morris
;  APPLICANT:  Marc Malandro
;  TITLE OF INVENTION: Novel Compositions and Methods in Cancer
;  FILE REFERENCE: CHIR0056-101 (PP023367.0003)
;  CURRENT APPLICATION NUMBER: US/10/540,898
;  CURRENT FILING DATE:  2005-06-27
;  PRIOR APPLICATION NUMBER: US 10/330,773
;  PRIOR FILING DATE: 2002-12-27
;  NUMBER OF SEQ ID NOS: 981
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 921
;   LENGTH: 348
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-540-898-921

  Query Match           87.5%;  Score 1633.5;  DB 6;  Length 348;
  Best Local Similarity  88.7%;  Pred. No. 1.4e-146;
  Matches  314;  Conservative   19;  Mismatches   12;  Indels    9;  Gaps    3;

Qy          6 VSIYTSDNYSEEVGSGDYDSNKEPCFRDENVHFNRIFLPTIYFIIFLTGIVGNGLVILVM 65
              :||||||||:||:||||||| |||||:|| :|||:||||||| ||||||||||||||||
Db          4 ISIYTSDNYTEEMGSGDYDSMKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVM 63

Qy         66 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAMADWYFGKFLCKAVHIIYTVNLYSS 125
              |||||||||||||||||||||||||||||||||:|:|||| |||||||:|||||   |
Db         64 GYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVN--KS 121

Qy        126 VLILAFISLDRYLAIVHATNSQRPRKLLAEKAVYVGVWIPALLLTIPDFIFADVSQGDIS 185
              |||||||||||||||||||||||||||||| ||||||||||||||||||:|     |
Db        122 VLILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFANV-----S 176

Qy        186 QGDDRYICDRLYPDSLWMVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 245
              : |||||||| ||: ||:||||||||||||||||||||||||||||||||||||||||||
Db        177 EADDRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKAL 236

Qy        246 KTTVILILAFFACWLPYYVGISIDSFILLGVIKQGCDFESIVHKWISITEALAFFHCCLN 305
              |||||||||||||||||:|||||||||| :|||||:||: |||||||||  ||||||||
Db        237 KTTVILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITE--AFFHCCLN 294

Qy        306 PILYAFLGAKFKSSAQHALNSMSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 359
              |||||||||||:|||||| |:||||||||||||||||||||||||||||||||
Db        295 PILYAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSFHSS 348

Search completed: February  6, 2007, 14:31:23
Job time : 42.4037 secs
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SCORE 1.3 BuildDate: 11/17/2006